



PR 20-OCT-1999: 99US-0160588.  
XX (UYMC-) UNIV MCGILL.  
PA (HOP-) HOPITAL SAINTE-JUSTINE.  
XX  
XX  
PI Hudson TJ, Engert J, Richter A;  
XX  
XX MPI: 2001-308494/32.  
DR P-PSDB; AAB97821.  
XX  
XX New isolated polynucleotide, encoding spastin gene, and polypeptides,  
PT useful for diagnosing autosomal recessive spastic ataxia of  
PT Charlevoix-Saguenay disease by detecting two point mutations in spastin  
PT gene sequence -  
XX  
XX Claim 1: Page -; 76pp: English.  
XX  
XX The present invention describes human and mouse spastin, and mutated  
CC human spastin (autosomal recessive spastic ataxia of Charlevoix-Saguenay  
CC (ARSA) gene sequences (I). The spastin gene has been mapped to  
CC chromosome 13q11. (I) have neuroprotective activities and can be used in  
CC gene therapy and as a spastin polypeptide agonists. (I), their fragments  
CC or their complements can be useful for assaying the presence of a nucleic  
CC acid molecule in a sample. (I) is useful for diagnosing or aiding in the  
CC diagnosis of an early onset neurodegenerative disease in an individual.  
CC The neurodegenerative disease comprises reduced sensory nerve conduction,  
CC reduced motor nerve velocity, hypermyelination of retinal nerve fibres,  
CC atrophy of upper cerebellar vermis, absence of Purkinje cells and  
CC abnormal neuronal lipid storage. (I) can also be used to produce  
CC antisense nucleic acids, is useful as molecular weight or chromosome  
CC markers, to identify genetic disorders, as hybridisation probes or  
CC primers, as an antigen, identify and express recombinant protein for  
CC analysis, characterisation or therapeutic use, or as markers for tissues  
CC in which the corresponding protein is expressed. Diagnostic methods from  
CC the present invention can be used to identify subjects having or at risk  
CC of developing a disease or disorder associated with aberrant expression  
CC or activity of (I). The assays can be utilised to identify a subject  
CC having or at risk of developing a disorder associated with Spastin  
CC protein or spastin gene expression or activity. The present sequence  
CC encodes a mutated human spastin.  
CC N.B. The present sequence is not given in the present specification but  
CC is derived from the human spastin nucleotide sequence (AAH20174) as  
CC stated on page 14.  
XX  
XX SQ Sequence 12792 BP; 4163 A; 2256 C; 2487 G; 3886 T; 0 other;  
Query Match 100.0%; Score 103; DB 22; Length 12792;  
Best Local Similarity 100.0%; Pred. No. 5.4e-23;  
Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GAAGTACTGGAATTAACAGTTTAATGACAGCATTAATAGCTCCATATGTAATGCT 60  
DB 6543 GAAGTACTGGAATTAACAGTTTAATGACAGCATTAATAGCTCCATATGTAATGCT 6602  
QY 61 AATACAGTTAAAAAAGCGTATTTCCTGCTGTTCTATCCACA 103  
DB 6603 AATACAGTTAAAAAAGCGTATTTCCTGCTGTTCTATCCACA 6645

RESULT 2  
AAH20174  
ID AAH20174 standard: DNA; 12793 BP.  
XX  
XX AAH20174;  
XX  
XX 09-AUG-2001 (first entry)  
XX  
XX Human spastin nucleotide sequence SEQ ID NO:1.  
XX  
XX Human; mouse; spastin; ARSACS; chromosome 13q11; identification;  
KW autosomal recessive spastic ataxia of Charlevoix-Saguenay; mutation;  
KW neurodegenerative disease; reduced sensory nerve conduction; diagnosis;  
KW reduced motor nerve velocity; hypermyelination of retinal nerve fibre;

KW atrophy of upper cerebellar vermis; absence of Purkinje cell;  
KW abnormal neuronal lipid storage; genetic disorder; characterisation; ds.  
XX  
XX Homo sapiens.  
OS  
XX  
XX  
FH Key Location/Qualifiers  
FT CDS 77..1156  
FT /tag= a  
FT /product= "spastin"  
XX  
XX MO200129266-A2.  
XX  
XX 26-APR-2001.  
XX  
XX 20-OCT-2000; 2000MO-US29130.  
XX  
XX  
XX 20-OCT-1999: 99US-0160588.  
XX  
XX  
XX (UYMC-) UNIV MCGILL.  
PA (HOP-) HOPITAL SAINTE-JUSTINE.  
PI Hudson TJ, Engert J, Richter A;  
XX  
XX MPI: 2001-308494/32.  
DR P-PSDB; AAB97819.  
XX  
XX New isolated polynucleotide, encoding spastin gene, and polypeptides,  
PT useful for diagnosing autosomal recessive spastic ataxia of  
PT Charlevoix-Saguenay disease by detecting two point mutations in spastin  
PT gene sequence -  
XX  
XX Claim 1: Fig 9; 76pp: English.  
XX  
XX The present invention describes human and mouse spastin, and mutated  
CC human spastin (autosomal recessive spastic ataxia of Charlevoix-Saguenay  
CC (ARSA) gene sequences (I). The spastin gene has been mapped to  
CC chromosome 13q11. (I) have neuroprotective activities and can be used in  
CC gene therapy and as a spastin polypeptide agonists. (I), their fragments  
CC or their complements can be useful for assaying the presence of a nucleic  
CC acid molecule in a sample. (I) is useful for diagnosing or aiding in the  
CC diagnosis of an early onset neurodegenerative disease in an individual.  
CC The neurodegenerative disease comprises reduced sensory nerve conduction,  
CC reduced motor nerve velocity, hypermyelination of retinal nerve fibres,  
CC atrophy of upper cerebellar vermis, absence of Purkinje cells and  
CC abnormal neuronal lipid storage. (I) can also be used to produce  
CC antisense nucleic acids, is useful as molecular weight or chromosome  
CC markers, to identify genetic disorders, as hybridisation probes or  
CC primers, as an antigen, identify and express recombinant protein for  
CC analysis, characterisation or therapeutic use, or as markers for tissues  
CC in which the corresponding protein is expressed. Diagnostic methods from  
CC the present invention can be used to identify subjects having or at risk  
CC of developing a disease or disorder associated with aberrant expression  
CC or activity of (I). The assays can be utilised to identify a subject  
CC having or at risk of developing a disorder associated with Spastin  
CC protein or spastin gene expression or activity. The present sequence  
CC encodes human spastin as given in the present invention.  
XX  
XX SQ Sequence 12793 BP; 4163 A; 2256 C; 2487 G; 3887 T; 0 other;  
Query Match 53.6%; Score 55.2; DB 22; Length 12793;  
Best Local Similarity 75.0%; Pred. No. 8.9e-08;  
Matches 69; Conservative 0; Mismatches 23; Indels 0; Gaps 0;  
QY 1 GAAGTACTGGAATTAACAGTTTAATGACAGCATTAATAGCTCCATATGTAATGCT 60  
DB 6543 GAAGTACTGGAATTAACAGTTTAATGACAGCATTAATAGCTCCATATGTAATGCT 6602  
QY 61 AATACAGTTAAAAAAGCGTATTTCCTGCTGTTCTATCCACA 92  
DB 6603 TAATACAGTTAAAAAAGCGTATTTCCTGCTGTTCTATCCACA 6634

RESULT 3

AAH20178  
ID AAH20178 standard; DNA: 12793 BP.  
XX  
AC AAH20178:  
XX  
DT 09-AUG-2001 (first entry)  
XX  
DE Human mutated spastin nucleotide sequence SEQ ID NO:11.  
XX  
KM Human: mouse; spastin; ARSACS; chromosome 13q11; identification;  
KM autosomal recessive spastic ataxia of Charlevoix-Saguenay; mutation;  
KM neurodegenerative disease; reduced sensory nerve conduction; diagnosis;  
KM reduced motor nerve velocity; hypermyelination of retinal nerve fibre;  
KM atrophy of upper cerebellar vermis; absence of Purkinje cell;  
KM abnormal neuronal lipid storage; genetic disorder; characterisation; ds.  
XX  
OS Homo sapiens.  
OS Synthetic.  
PN WO200129266-A2.  
XX  
PD 26-APR-2001.  
XX  
PF 20-OCT-2000; 2000WO-US29130.  
XX  
PR 20-OCT-1999; 99US-0160588.  
XX  
PA (UYMC-) UNIV MCGILL.  
PA (HOPIT-) HOPITAL SAINTE-JUSTINE.  
XX  
PI Hudson TJ, Engert J, Richter A;  
XX  
DR WPI: 2001-308494/32.  
XX  
PT New isolated polynucleotide, encoding spastin gene, and polypeptides,  
PT useful for diagnosing autosomal recessive spastic ataxia of  
PT Charlevoix-Saguenay disease by detecting two point mutations in spastin  
PT gene sequence -  
XX  
PS Claim 1; Page -: 76pp; English.  
XX  
CC The present invention describes human and mouse spastin, and mutated  
CC human spastin (autosomal recessive spastic ataxia of Charlevoix-Saguenay  
CC (ARSACS)) gene sequences (I). The spastin gene has been mapped to  
CC chromosome 13q11. (I) have neuroprotective activities and can be used in  
CC gene therapy and as a spastin polypeptide agonists. (II), their fragments  
CC or their complements can be useful for assaying the presence of a nucleic  
CC acid molecule in a sample. (I) is useful for diagnosing or aiding in the  
CC diagnosis of an early onset neurodegenerative disease in an individual.  
CC The neurodegenerative disease comprises reduced sensory nerve conduction,  
CC reduced motor nerve velocity, hypermyelination of retinal nerve fibres,  
CC atrophy of upper cerebellar vermis, absence of Purkinje cells and  
CC abnormal neuronal lipid storage. (I) can also be used to produce  
CC antisense nucleic acids, is useful as molecular weight or chromosome  
CC markers, to identify genetic disorders, as hybridisation probes or  
CC primers, as an antigen, identify and express recombinant protein for  
CC analysis, characterisation or therapeutic use, or as markers for tissues  
CC in which the corresponding protein is expressed. Diagnostic methods from  
CC the present invention can be used to identify subjects having or at risk  
CC of developing a disease or disorder associated with aberrant expression  
CC or activity of (I). The assays can be utilised to identify a subject  
CC having or at risk of developing a disorder associated with Spastin  
CC protein or spastin gene expression or activity. The present sequence  
CC represents a mutated human spastin gene from the present invention.  
CC N.B. The present sequence is not given in the present specification but  
CC is derived from the human spastin nucleotide sequence (AAH20174) as  
CC stated on page 14.  
XX  
SO Sequence 12793 BP; 4163 A; 2255 C; 2487 G; 3888 T; 0 other;

Query Match 53.68; Score 55.2; DB 22; Length 12793;  
Best Local Similarity 75.08; Pred. No. 8.9e-08;  
Matches 69; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

0Y 1 GAAGTGACGTGAATACAGTTTAAATGACAGATTATAGCTCATATGTAATTGCT 60  
DB 6543 GAACTGACTGGAATACAGTTTAAATGACAGATTATAGCTCATATGTAATTGC 6602  
0Y 61 AATACAGTTAAAAAAGCGTATTTCCCTGGTT 92  
DB 6603 TAAATACAGTTAAAAAAGCGTATTTCCCTGGT 6634

RESULT 4  
AAH20179  
ID AAH20179 standard; DNA: 12793 BP.  
XX  
AC AAH20179;  
XX  
DT 09-AUG-2001 (first entry)  
XX  
DE Human mutated spastin nucleotide sequence SEQ ID NO:12.  
XX  
KM Human: mouse; spastin; ARSACS; chromosome 13q11; identification;  
KM autosomal recessive spastic ataxia of Charlevoix-Saguenay; mutation;  
KM neurodegenerative disease; reduced sensory nerve conduction; diagnosis;  
KM reduced motor nerve velocity; hypermyelination of retinal nerve fibre;  
KM atrophy of upper cerebellar vermis; absence of Purkinje cell;  
KM abnormal neuronal lipid storage; genetic disorder; characterisation; ds.  
XX  
OS Homo sapiens.  
OS Synthetic.  
PN WO200129266-A2.  
XX  
PD 26-APR-2001.  
XX  
PF 20-OCT-2000; 2000WO-US29130.  
XX  
PR 20-OCT-1999; 99US-0160588.  
XX  
PA (UYMC-) UNIV MCGILL.  
PA (HOPIT-) HOPITAL SAINTE-JUSTINE.  
XX  
PI Hudson TJ, Engert J, Richter A;  
XX  
DR WPI: 2001-308494/32.  
XX  
PT New isolated polynucleotide, encoding spastin gene, and polypeptides,  
PT useful for diagnosing autosomal recessive spastic ataxia of  
PT Charlevoix-Saguenay disease by detecting two point mutations in spastin  
PT gene sequence -  
XX  
PS Claim 1; Page -: 76pp; English.  
XX  
CC The present invention describes human and mouse spastin, and mutated  
CC human spastin (autosomal recessive spastic ataxia of Charlevoix-Saguenay  
CC (ARSACS)) gene sequences (I). The spastin gene has been mapped to  
CC chromosome 13q11. (I) have neuroprotective activities and can be used in  
CC gene therapy and as a spastin polypeptide agonists. (II), their fragments  
CC or their complements can be useful for assaying the presence of a nucleic  
CC acid molecule in a sample. (I) is useful for diagnosing or aiding in the  
CC diagnosis of an early onset neurodegenerative disease in an individual.  
CC The neurodegenerative disease comprises reduced sensory nerve conduction,  
CC reduced motor nerve velocity, hypermyelination of retinal nerve fibres,  
CC atrophy of upper cerebellar vermis, absence of Purkinje cells and  
CC abnormal neuronal lipid storage. (I) can also be used to produce  
CC antisense nucleic acids, is useful as molecular weight or chromosome  
CC markers, to identify genetic disorders, as hybridisation probes or  
CC primers, as an antigen, identify and express recombinant protein for  
CC analysis, characterisation or therapeutic use, or as markers for tissues  
CC in which the corresponding protein is expressed. Diagnostic methods from  
CC the present invention can be used to identify subjects having or at risk  
CC of developing a disease or disorder associated with aberrant expression  
CC or activity of (I). The assays can be utilised to identify a subject  
CC having or at risk of developing a disorder associated with Spastin

CC protein or spastin gene expression or activity. The present sequence  
CC encodes a mutated human spastin.  
CC N.B. The present sequence is not given in the present specification but  
CC is derived from the human spastin nucleotide sequence (AAH20174) as  
CC stated on page 14.  
XX  
SQ Sequence 12793 BP; 4163 A; 2257 C; 2487 G; 3886 T; 0 other:  
Query Match 53.6%; Score 55.2; DB 22; Length 12793;  
Best Local Similarity 75.0%; Pred. No. 8.9e-08;  
Matches 69; Conservative 0; Mismatches 23; Indels 0; Gaps 0;  
OY 1 GAAGTGACTGGAATAACACTTTAATGACAGCATTAATACCTCGCATATGCAATTGCT 60  
DB 6543 GAAGTGACTGGAATAACACTTTAATGACAGCATTAATACCTCGCATATGTTGAATTGC 6602  
OY 61 AATACAGTTAAAAAAGCGTATTTCCCTGCT 92  
DB 6603 CATATACAGTTAAAAAAGCGTATTTCCCTGCT 6634  
RESULT 5  
AAH20182  
ID AAH20182 standard; DNA; 12793 BP.  
XX  
AC AAH20182;  
XX  
DT 09-AUG-2001 (first entry)  
XX  
DE Human mutated spastin nucleotide sequence SEQ ID NO:15.  
XX  
KW Human; mouse; spastin; ARSACS; chromosome 13q11; identification;  
KW autosomal recessive spastic ataxia of Charlevoix-Saguenay; mutation;  
KW neurodegenerative disease; reduced sensory nerve conduction; diagnosis;  
KW reduced motor nerve velocity; hypermyelination of retinal nerve fibre;  
KW atrophy of upper cerebellar vermis; absence of Purkinje cell;  
KW abnormal neuronal lipid storage; genetic disorder; characterisation; ds.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT CDS 77..11566  
FT /\*tag= a  
FT /\*product= "mutated spastin"  
XX  
XX WO200129266-A2.  
XX  
XX PD 26-APR-2001.  
XX  
XX PF 20-OCT-2000; 2000WO-US29130.  
XX  
XX PR 20-OCT-1999; 99US-0160588.  
XX  
XX PA (UWMC-) UNIV MCGILL.  
XX (HOPIT- ) HOPITAL SAINTE-JUSTINE.  
XX  
XX PI Hudson TJ, Engert J, Richter A;  
XX  
XX DR WPI; 2001-308494/32.  
XX P-PSDB; AAB97823.  
XX  
XX PT New isolated polynucleotide, encoding spastin gene, and polypeptides,  
XX useful for diagnosing autosomal recessive spastic ataxia of  
XX Charlevoix-Saguenay disease by detecting two point mutations in spastin  
XX gene sequence -  
XX  
XX PS Claim 1; Page -: 76pp; English.  
XX  
XX CC The present invention describes human and mouse spastin, and mutated  
XX human spastin (autosomal recessive spastic ataxia of Charlevoix-Saguenay  
XX (ARSACS)) gene sequences (1). The spastin gene has been mapped to  
XX chromosome 13q11. (1) have neuroprotective activities and can be used in

CC gene therapy and as a spastin polypeptide agonists. (1), their fragments  
CC or their complements can be useful for assaying the presence of a nucleic  
CC acid molecule in a sample. (1) is useful for diagnosing or aiding in the  
CC diagnosis of an early onset neurodegenerative disease in an individual.  
CC The neurodegenerative disease comprises reduced sensory nerve conduction,  
CC reduced motor nerve velocity, hypermyelination of retinal nerve fibres,  
CC atrophy of upper cerebellar vermis, absence of Purkinje cells and  
CC abnormal neuronal lipid storage. (1) can also be used to produce  
CC antisense nucleic acids, is useful as molecular weight or chromosome  
CC markers, to identify genetic disorders, as hybridisation probes or  
CC primers, as an antigen, identify and express recombinant protein for  
CC analysis, characterisation or therapeutic use, or as markers for tissues  
CC in which the corresponding protein is expressed. Diagnostic methods from  
CC the present invention can be used to identify subjects having or at risk  
CC of developing a disease or disorder associated with aberrant expression  
CC or activity of (1). The assays can be utilised to identify a subject  
CC having or at risk of developing a disorder associated with Spastin  
CC protein or spastin gene expression or activity. The present sequence  
CC encodes a mutated human spastin.  
CC N.B. The present sequence is not given in the present specification but  
CC is derived from the human spastin nucleotide sequence (AAH20174) as  
CC stated on page 14.  
XX  
SQ Sequence 12793 BP; 4163 A; 2257 C; 2487 G; 3886 T; 0 other:  
Query Match 53.6%; Score 55.2; DB 22; Length 12793;  
Best Local Similarity 75.0%; Pred. No. 8.9e-08;  
Matches 69; Conservative 0; Mismatches 23; Indels 0; Gaps 0;  
OY 1 GAAGTGACTGGAATAACACTTTAATGACAGCATTAATACCTCGCATATGCAATTGCT 60  
DB 6543 GAAGTGACTGGAATAACACTTTAATGACAGCATTAATACCTCGCATATGTTGAATTGC 6602  
OY 61 AATACAGTTAAAAAAGCGTATTTCCCTGCT 92  
DB 6603 TAATACAGTTAAAAAAGCGTATTTCCCTGCT 6634  
RESULT 6  
AAH20175  
ID AAH20175 standard; DNA; 11493 BP.  
XX  
AC AAH20175;  
XX  
DT 09-AUG-2001 (first entry)  
XX  
DE Mouse spastin nucleotide sequence SEQ ID NO:3.  
XX  
XX KW Human; mouse; spastin; ARSACS; chromosome 13q11; identification;  
XX KW autosomal recessive spastic ataxia of Charlevoix-Saguenay; mutation;  
XX KW neurodegenerative disease; reduced sensory nerve conduction; diagnosis;  
XX KW reduced motor nerve velocity; hypermyelination of retinal nerve fibre;  
XX KW atrophy of upper cerebellar vermis; absence of Purkinje cell;  
XX KW abnormal neuronal lipid storage; genetic disorder; characterisation; ds.  
XX  
XX OS Mus musculus.  
XX  
XX FH Key Location/Qualifiers  
FT CDS 1..11493  
FT /\*tag= a  
FT /\*product= "spastin"  
XX  
XX WO200129266-A2.  
XX  
XX PD 26-APR-2001.  
XX  
XX PF 20-OCT-2000; 2000WO-US29130.  
XX  
XX PR 20-OCT-1999; 99US-0160588.  
XX  
XX PA (UWMC-) UNIV MCGILL.  
XX (HOPIT- ) HOPITAL SAINTE-JUSTINE.  
XX



PI Hudson TJ, Engert J, Richter A;  
XX  
DR WPI: 2001-308494/32.  
DR P-PSDB; AAB97820.  
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PT useful for diagnosing autosomal recessive spastic ataxia of  
PT Charlevoix-Saguenay disease by detecting two point mutations in spastin  
PT gene sequence -  
XX  
PS Claim 1; Fig 8; 76pp; English.  
XX  
CC The present invention describes human and mouse spastin, and mutated  
CC spastin (autosomal recessive spastic ataxia of Charlevoix-Saguenay  
CC (ARSA)) gene sequences (I). The spastin gene has been mapped to  
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CC gene therapy and as a spastin polypeptide agonists. (II), their fragments  
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CC diagnosis of an early onset neurodegenerative disease in an individual.  
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CC atrophy of upper cerebellar vermis, absence of Purkinje cells and  
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CC markers, to identify genetic disorders, as hybridisation probes or  
CC primers, as an antigen, identify and express recombinant protein for  
CC analysis, characterisation or therapeutic use, or as markers for tissues  
CC in which the corresponding protein is expressed. Diagnostic methods from  
CC the present invention can be used to identify subjects having or at risk  
CC of developing a disease or disorder associated with aberrant expression  
CC or activity of (I). The assays can be utilised to identify a subject  
CC having or at risk of developing a disorder associated with Spastin  
CC protein or spastin gene expression or activity. The present sequence  
CC encodes mouse spastin as given in the present invention.  
XX  
SQ Sequence 11493 BP; 3599 A; 2281 C; 2387 G; 3226 T; 0 other;  
XX  
Query Match 52.0%; Score 53.6; DB 22; Length 11493;  
Best Local Similarity 73.9%; Pred. No. 2.8e-07;  
Matches 68; Conservative 0; Mismatches 24; Indels 0; Gaps 0;  
OY 1 GAAGTGCATGGAATTAACAGTTTAATGACACATTAAATAGCTCGATATGGAATTGCT 60  
DB 6467 GAAGTGCATGGAATTAATAGTTTAATGACACATTAAATAGACACCTGATGCTTAC 6526  
OY 61 AATACAGTTAAAAAAGCGTATTTCCCTGGT 92  
DB 6527 TAATCCAGTTAAAAAAGCGTATTTCCCTGGT 6558  
RESULT 7  
AAS42107 standard; DNA; 1541 BP.  
XX  
AC AAS42107;  
XX  
DT 17-Dec-2001 (first entry)  
XX  
DE Genomic sequence #423 encoding novel human enzyme polypeptide.  
XX  
KW Human: oxidoreductase enzyme; transferase; hydrolase; lyase; isomerase;  
KW ligase; hyperproliferative disorder; immunodeficiency disorder;  
KW autoimmune disorder; neurological disorder; metabolic disorder;  
KW inflammatory disorder; cardiovascular disorder; reproductive disorder;  
KW blood-related disorder; infectious disorder; gene therapy; cytostatic;  
KW anti arthritic; nephrotropic; anticoagulant; ds.  
XX  
OS Homo sapiens.  
XX  
XX WO200155301-A2.  
XX  
XX 02-AUG-2001.  
PD

XX  
PF 17-JAN-2001; 2001WO-US01239.  
XX  
PR 31-JAN-2000; 2000US-0179065.  
PR 04-FEB-2000; 2000US-0180628.  
PR 24-FEB-2000; 2000US-0184664.  
PR 02-MAR-2000; 2000US-0186350.  
PR 16-MAR-2000; 2000US-0189874.  
PR 17-MAR-2000; 2000US-0190076.  
PR 18-APR-2000; 2000US-0198123.  
PR 19-MAY-2000; 2000US-0205515.  
PR 07-JUN-2000; 2000US-0209467.  
PR 28-JUN-2000; 2000US-0214886.  
PR 30-JUN-2000; 2000US-0215135.  
PR 07-JUL-2000; 2000US-0216647.  
PR 07-JUL-2000; 2000US-0216880.  
PR 11-JUL-2000; 2000US-0217487.  
PR 11-JUL-2000; 2000US-0217496.  
PR 14-JUL-2000; 2000US-0218290.  
PR 26-JUL-2000; 2000US-0220963.  
PR 26-JUL-2000; 2000US-0220964.  
PR 14-AUG-2000; 2000US-0224518.  
PR 14-AUG-2000; 2000US-0224519.  
PR 14-AUG-2000; 2000US-0225213.  
PR 14-AUG-2000; 2000US-0225214.  
PR 14-AUG-2000; 2000US-0225266.  
PR 14-AUG-2000; 2000US-0225267.  
PR 14-AUG-2000; 2000US-0225268.  
PR 14-AUG-2000; 2000US-0225270.  
PR 14-AUG-2000; 2000US-0225447.  
PR 14-AUG-2000; 2000US-0225757.  
PR 14-AUG-2000; 2000US-0225758.  
PR 14-AUG-2000; 2000US-0225759.  
PR 18-AUG-2000; 2000US-0226279.  
PR 22-AUG-2000; 2000US-0226681.  
PR 22-AUG-2000; 2000US-0226868.  
PR 22-AUG-2000; 2000US-0227182.  
PR 23-AUG-2000; 2000US-0227009.  
PR 30-AUG-2000; 2000US-0228924.  
PR 01-SEP-2000; 2000US-0229287.  
PR 01-SEP-2000; 2000US-0229343.  
PR 01-SEP-2000; 2000US-0229344.  
PR 01-SEP-2000; 2000US-0229345.  
PR 05-SEP-2000; 2000US-0229509.  
PR 05-SEP-2000; 2000US-0229513.  
PR 06-SEP-2000; 2000US-0230437.  
PR 06-SEP-2000; 2000US-0230438.  
PR 08-SEP-2000; 2000US-0231242.  
PR 08-SEP-2000; 2000US-0231243.  
PR 08-SEP-2000; 2000US-0231244.  
PR 08-SEP-2000; 2000US-0231413.  
PR 08-SEP-2000; 2000US-0231414.  
PR 08-SEP-2000; 2000US-0232080.  
PR 08-SEP-2000; 2000US-0232081.  
PR 12-SEP-2000; 2000US-0231968.  
PR 14-SEP-2000; 2000US-0232397.  
PR 14-SEP-2000; 2000US-0232398.  
PR 14-SEP-2000; 2000US-0232399.  
PR 14-SEP-2000; 2000US-0232400.  
PR 14-SEP-2000; 2000US-0232401.  
PR 14-SEP-2000; 2000US-0233063.  
PR 14-SEP-2000; 2000US-0233064.  
PR 14-SEP-2000; 2000US-0233065.  
PR 21-SEP-2000; 2000US-0234223.  
PR 21-SEP-2000; 2000US-0234274.  
PR 25-SEP-2000; 2000US-0234997.  
PR 25-SEP-2000; 2000US-0234998.  
PR 26-SEP-2000; 2000US-0235484.  
PR 27-SEP-2000; 2000US-0235834.  
PR 27-SEP-2000; 2000US-0235836.  
PR 29-SEP-2000; 2000US-0236327.  
PR 29-SEP-2000; 2000US-0236367.  
PR 29-SEP-2000; 2000US-0236368.

[illegible]

FT	variation	/note="Polymorphic site 3"	FT	variation	replace (33671, C)
FT		/tag= e	FT		/tag= x
FT		/standard_name="Single nucleotide polymorphism (SNP)"	FT		/standard_name="Single nucleotide polymorphism (SNP)"
FT		/note="Polymorphic site 4"	FT	exon	/note="Polymorphic site 21"
FT	variation	replace (11672, G)	FT		/tag= y
FT		/standard_name="Single nucleotide polymorphism (SNP)"	FT	intron	34144..35683
FT		/note="Polymorphic site 5"	FT		/tag= z
FT	variation	replace (11897, C)	FT	exon	35684..35737
FT		/tag= g	FT		/tag= aa
FT		/standard_name="Single nucleotide polymorphism (SNP)"	FT	intron	35738..39940
FT		/note="Polymorphic site 6"	FT		/tag= ab
FT	variation	replace (14523, C)	FT	variation	replace (37703, G)
FT		/tag= h	FT		/tag= ac
FT		/standard_name="Single nucleotide polymorphism (SNP)"	FT		/standard_name="Single nucleotide polymorphism (SNP)"
FT		/note="Polymorphic site 7"	FT	variation	replace (39263, G)
FT		replace (16586, T)	FT		/tag= ad
FT		/tag= i	FT		/standard_name="Single nucleotide polymorphism (SNP)"
FT		/standard_name="Single nucleotide polymorphism (SNP)"	FT		/note="Polymorphic site 23; This position is given
FT		/note="Polymorphic site 8"	FT	exon	as 39941..40038
FT	variation	replace (16644, C)	FT		/tag= ae
FT		/tag= j	FT	intron	40039..45810
FT		/standard_name="Single nucleotide polymorphism (SNP)"	FT		/tag= af
FT		/note="Polymorphic site 9"	FT	exon	45811..45871
FT	variation	replace (17969, G)	FT		/tag= ag
FT		/tag= k	FT	intron	45872..46578
FT		/standard_name="Single nucleotide polymorphism (SNP)"	FT		/tag= ah
FT		/note="Polymorphic site 10"	FT	exon	46579..46615
FT	variation	replace (18117, T)	FT		/tag= ai
FT		/tag= l	FT	intron	46616..47002
FT		/standard_name="Single nucleotide polymorphism (SNP)"	FT		/tag= aj
FT		/note="Polymorphic site 11"	FT	exon	47003..47042
FT	variation	replace (18518, A)	FT		/tag= ak
FT		/tag= m	FT	intron	47043..47133
FT		/standard_name="Single nucleotide polymorphism (SNP)"	FT		/tag= al
FT		/note="Polymorphic site 12"	FT	exon	47134..47184
FT	exon	19364..19420	FT		/tag= am
FT		/tag= n	FT	intron	47185..48943
FT		19421..34110	FT		/tag= an
FT	intron	replace (19882, A)	FT	exon	48944..49016
FT		/tag= o	FT		/tag= ao
FT	variation	/standard_name="Single nucleotide polymorphism (SNP)"	FT	intron	49017..57568
FT		/note="Polymorphic site 13"	FT		/tag= ap
FT	variation	replace (20988, -)	FT	exon	57569..57602
FT		/tag= q	FT		/tag= aq
FT		/standard_name="Single nucleotide polymorphism (SNP)"	FT	intron	57603..57761
FT		/note="Polymorphic site 14"	FT		/tag= ar
FT	variation	replace (20999, T)	FT	exon	57762..59835
FT		/tag= r	FT		/tag= as
FT		/standard_name="Single nucleotide polymorphism (SNP)"	XX		
FT		/note="Polymorphic site 15"	PN	MO200160992-A2.	
FT	variation	replace (21465, G)	XX		
FT		/tag= s	XX	23-AUG-2001.	
FT		/standard_name="Single nucleotide polymorphism (SNP)"	PD		
FT		/note="Polymorphic site 16"	XX		
FT	variation	replace (21625, T)	PE	12-FEB-2001; 2001MO-US04432.	
FT		/tag= t	XX		
FT		/standard_name="Single nucleotide polymorphism (SNP)"	PR	14-FEB-2000; 2000US-0182194.	
FT		/note="Polymorphic site 17"	XX	11-OCT-2000; 2000US-0685853.	
FT	variation	replace (26291, T)	XX		
FT		/tag= u	PA	(PEKE ) PE CORP NY.	
FT		/standard_name="Single nucleotide polymorphism (SNP)"	XX		
FT		/note="Polymorphic site 18"	PI	Wei M, Ketchum KA, Di Francesco V, Beasley EM;	
FT	variation	replace (28012, C)	XX		
FT		/tag= v	DR	WPI; 2001-529910/58.	
FT		/standard_name="Single nucleotide polymorphism (SNP)"	XX	P-PDB; AAE08552.	
FT	variation	replace (28030, G)	PT	New phosphatase peptide for the screening of modulators useful for	
FT		/tag= w	XX	treating related disorders -	
FT		/standard_name="Single nucleotide polymorphism (SNP)"	PS	Claim 4; Fig 3; 109pp; English.	
FT		/note="Polymorphic site 20"	XX		

CC The present invention provides phosphatase peptides, proteins and  
CC their polynucleotides. The phosphatase proteins are related to the  
CC protein tyrosine phosphatase subfamily. The peptides of the invention  
CC are useful for identifying a modulator of phosphatase peptide expression.  
CC Modulators of phosphatase peptide are useful for treating diseases or  
CC conditions mediated by a human phosphatase protein. The phosphatase gene  
CC of the present invention can be expressed in yeast to identify possible  
CC interactors and substrates. Artificially synthesised enzymes or derived  
CC peptides can be used to activate or inhibit cellular processes modulated  
CC by this phosphatase. The present sequence is a human gene encoding  
CC phosphatase protein. This gene is located on human chromosome 14.  
XX  
SQ Sequence 74962 BP; 21639 A; 14055 C; 14307 G; 24824 T; 137 other:  
Query Match 35.1%; Score 36.2; DB 22; Length 74962;  
Best Local Similarity 62.9%; Pred. No. 0.14;  
Matches 56; Conservative 0; Mismatches 33; Indels 0; Gaps 0;  
QY 12 AATACAGTTTATGACAGCATTTATACCTCTGATATGATGCTAATACAGTTAA 71  
DB 63338 AAAAAAAAAAATTCAGCATTCAGAGCCCTAGAGACTTACTTTCTAATCAATTTAA 63279  
QY 72 AAAAAAGCTATTTCCCTGCTCTGATCCA 100  
DB 63278 AAAAAAGCTTTTCAGTACTTCTCATCTA 63250  
RESULT 9  
ABST9021/C  
ID ABST9021 standard; DNA; 1604 BP.  
XX  
AC ABST9021;  
XX  
DT 17-DEC-2002 (first entry)  
XX  
DE E. coli CFT073 genomic sequence #188.  
XX  
KM Pathogenic; Escherichia coli CFT073 infection; livestock; pyelonephritis;  
KM urinary tract infection; open reading frame; ORF; uropathogenic;  
KM antibacterial; atrophic; nephrotropic; gene; ds.  
XX  
OS Escherichia coli.  
XX  
PN WO200259320-A2.  
XX  
PD 01-AUG-2002.  
XX  
PF 19-OCT-2001; 2001WO-US46833.  
XX  
PR 19-OCT-2000; 2000US-242412P.  
XX  
PA (WISC ) WISCONSIN ALUMNI RES FOUND.  
XX  
PI Blattner FR, Welch RA, Burland VD;  
XX  
DR WPI; 2002-691532/74.  
XX  
PT New DNA sequences of the pathogenic Escherichia coli CFT073 strain,  
PT useful for preventing or treating E. coli CFT073 infection in humans or  
PT livestock  
XX  
PS Claim 1; Page 566; 765pp; English.  
XX  
CC The present invention relates to polynucleotide sequences from the  
CC genome of the pathogenic Escherichia coli strain CFT073. Almost all  
CC the sequences present in E. coli CFT073 are absent in the previously  
CC sequenced laboratory strain K-12. The polynucleotide sequences of  
CC the invention are useful for preventing, diagnosing or treating  
CC E. coli CFT073 infection in humans or livestock. The polynucleotide  
CC sequences are useful for preventing urinary tract infections and  
CC pyelonephritis. Likewise, the polypeptides encoded by the different  
CC open reading frames (ORF1-5) are useful for generating a vaccine  
CC against uropathogenic E. coli strains. ABST9834-ABST9085 represent

CC genomic sequences from E. coli strain CFT073.  
XX  
SQ Sequence 1604 BP; 534 A; 247 C; 276 G; 547 T; 0 other:  
QY  
Query Match 30.7%; Score 31.6; DB 24; Length 1604;  
Best Local Similarity 56.9%; Pred. No. 1.9;  
Matches 58; Conservative 0; Mismatches 44; Indels 0; Gaps 0;  
QY 2 AAGTCACTGGAATACAGTTTATGACAGCATTTATACCTCTGATATGATGCTA 61  
DB 1130 AAGTCAATGATATGATATTTTATTTTGCAAAATGAAAGATCTGCAAAATCTTCTT 1071  
QY 62 ATACAGTAAAAAAGGTATTTCCCTGCTCTGATCCAACA 103  
DB 1070 TTTTGACAAATACAAACATCATCAGGATCTGATGATCA 1029  
RESULT 10  
ABQ75995/C  
ID ABQ75995 standard; DNA; 31412 BP.  
XX  
AC ABQ75995;  
XX  
DT 05-NOV-2002 (first entry)  
XX  
DE Sheep PRP gene nucleic acid sequence.  
XX  
KM Sheep; PRP; prion; transmissible spongiform encephalopathy; TSE; scrapie;  
KM breeding; selection; gene; ds.  
XX  
OS Ovis aries.  
XX  
PN GB2371048-A.  
XX  
PD 17-JUL-2002.  
XX  
PF 10-JAN-2001; 2001GB-0000702.  
XX  
PR 10-JAN-2001; 2001GB-0000702.  
XX  
PA (UYYO-) UNIV YORK.  
XX  
PI Ross J, Bowles D;  
XX  
DR WPI; 2002-577556/62.  
XX  
PT Assay for comparing nucleic acid sequence with a reference, useful for  
PT determining prion gene alleles, comprises determining the profile of  
PT heteroduplexes  
XX  
PS Claim 2 (1)(a); Fig 1; 36pp; English.  
XX  
CC The invention relates to an assay for determining allelic variations in  
CC prion protein genes, involving comparing a nucleic acid sequence with a  
CC reference. The method is used for determining the PRP allele in an animal  
CC (or human) in order to assess susceptibility to transmissible spongiform  
CC encephalopathies (TSE), most especially scrapie in sheep. This assists in  
CC the selection, for breeding, of animals having the alleles known to be  
CC associated with lowest risk. The method is reproducible and rapid,  
CC provides high resolution between allelic variants and is suitable for  
CC processing large numbers of samples. The current sequence represents a  
CC sheep PRP gene, that is used in the context of the invention as a  
CC comparison nucleic acid.  
XX  
SQ Sequence 31412 BP; 8889 A; 6517 C; 6464 G; 9542 T; 0 other:  
Query Match 28.5%; Score 29.4; DB 24; Length 31412;  
Best Local Similarity 63.4%; Pred. No. 17;  
Matches 45; Conservative 0; Mismatches 26; Indels 0; Gaps 0;  
QY 13 ATACAGTTTATGACAGCATTTATACCTCTGATATGATGCTAATACAGTTAA 72  
DB 21603 ATATCTGTTAAATGAAAGAAATTAACATCTCTCAACATTAATGACCAAGAAATTTTA 21544



```
FT /tag= t
FT /number= 10
FT Intron 132923..133775
FT /tag= u
FT /number= 10
FT exon 133776..133848
FT /tag= v
FT /number= 11
FT Intron 133849..134127
FT /tag= w
FT /number= 11
FT exon 134128..134155
FT /tag= x
FT /number= 12
FT Intron 134156..134530
FT /tag= y
FT /number= 12
FT exon 134531..134545
FT /tag= z
FT /number= 13
FT Intron 134546..135588
FT /tag= aa
FT /number= 13
FT exon 135589..135601
FT /tag= ab
FT /number= 14
FT Intron 135602..137397
FT /tag= ac
FT /number= 14
FT exon 137398..137526
FT /tag= ad
FT /number= 15
FT Intron 137527..145751
FT /tag= ae
FT /number= 15
FT exon 145752..145816
FT /tag= af
FT /number= 16
FT Intron 145817..146200
FT /tag= ag
FT /number= 16
FT exon 146201..146291
FT /tag= ah
FT /number= 17
FT variation replace (210, A)
FT /tag= ai
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT /tag= aj
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT /tag= ak
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT /tag= al
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT /tag= am
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT /tag= an
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT /tag= ao
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT /tag= ap
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT /tag= aq
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT /tag= ar
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT /tag= at
```

```
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT replace (6048, T)
FT /tag= as
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT /tag= at
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT /tag= au
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT /tag= av
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT /tag= aw
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT /tag= ax
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT /tag= ay
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT /tag= az
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT /tag= ba
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT /tag= bb
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT /tag= bc
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT /tag= bd
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT /tag= be
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT /tag= bf
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT /tag= bg
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT /tag= bh
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT /tag= bi
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT /tag= bj
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT /tag= bk
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Query Match 28.3%; Score 29.2; DB 25; Length 148567;

Best local Similarity 56.1%; Pred. 27;

Matches 55; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

```
QY 5 TGACGTGGAATTAACAGTTTAATGACAGCAATTAAGCTCGATATGTAATGCTAATA 64
DB 73685 TGCATTGCATTATATGTAATTAACCAATTAATATTTCTTTGCGCTGAATGCTCACT 73626
QY 65 CAGTTAAANAACGGTATTTCCCTGGTGTGATCCAAC 102
DB 73625 AATTGAACAAGAAATTTGTGCGCTGCTCATTCTTAAC 73588
```

RESULT 13  
ABV53300  
ID ABV53300 standard; cDNA; 594 BP.  
XX  
AC ABV53300;





XX 24-OCT-1996.  
 PD 22-APR-1996; 96WO-US05320.  
 XX  
 XX  
 XX 07-JUN-1995; 95US-0487429.  
 PR 21-APR-1995; 95US-0426787.  
 PR 07-JUN-1995; 95US-0476102.  
 XX  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 PA (UYJO ) UNIV JOHNS HOPKINS.  
 XX  
 PI Adams MD, Fleischmann RD, Smith HO, Venter JC, White O;  
 XX WPI; 1996-485782/48.  
 DR  
 XX  
 PT Haemophilus influenzae Rd genome recorded on computer readable  
 PT medium - useful for identifying commercially important nucleic acid  
 PT fragments by homology searching  
 XX  
 XX Claim 1; Page 77.2-77.1091; 1291pp; English.  
 PS  
 XX  
 CC This sequence represents the complete genome sequence of the bacterium  
 CC Haemophilus influenzae strain Rd. The invention relates to a computer  
 CC readable medium (CRM) having recorded upon it the complete H. influenzae  
 CC nucleotide sequence (I), a representative fragment of (I) or a nucleotide  
 CC sequence at least 9% identical to (I). By providing the full-length  
 CC genomic sequence in a computer readable form, it is possible to identify  
 CC commercially important nucleic acid fragments and expression modulating  
 CC fragments (EMFs) of the Haemophilus genome. The EMFs can be used to  
 CC regulate the expression of a nucleic acid molecule. Vectors and altered  
 CC organisms comprising the predicted ORFs can be used to produce any of the  
 CC polypeptide fragments of the H. influenzae Rd genome.  
 XX  
 SQ Sequence 1830121 BP; 567399 A; 350615 C; 347389 G; 564036 T; 682 other;  
 Query Match 28.0%; Score 28.8; DB 17; Length 1830121;  
 Best Local Similarity 58.0%; Pred. No. 59;  
 Matches 51; Conservative 0; Mismatches 37; Indels 0; Gaps 0;  
 QY 13 ATACAGTTTAAATGACAGCATTAATAGCTCCGATATGATGATTAATACAGTTAA 72  
 DB 1541231 ATTAAGAGAGCTGTTTTCATTAATAGTTAGTGTATTTTCATTTTCATTTAA 1541172  
 QY 73 AAAACGGATTTTCCCTGTTTCATCA 100  
 DB 1541171 AAAATATATATTCCTCTATTCATCA 1541144  
 RESULT 16  
 ABL10204/C  
 ID ABL10204 standard; CDNA; 3631 BP.  
 XX  
 AC ABL10204;  
 XX  
 DT 26-MAR-2002 (first entry)  
 XX  
 XX Drosophila melanogaster expressed polynucleotide SEQ ID NO 25094.  
 DE  
 XX  
 XX Drosophila: developmental biology; cell signalling; insecticide;  
 KW pharmaceutical; gene; ss.  
 KW  
 XX Drosophila melanogaster.  
 OS  
 PN WO200171042-A2.  
 XX  
 PD 27-SEP-2001.  
 XX  
 XX 23-MAR-2001; 2001WO-US09231.  
 PF  
 XX 23-MAR-2000; 2000US-191637P.  
 PR 11-JUL-2000; 2000US-0614150.  
 XX

PA (PEKE ) PE CORP NY.  
 XX  
 XX Venter JC, Adams M, Li PWD, Myers EM;  
 PI  
 XX WPI; 2001-656860/75.  
 DR  
 DR P-PSDB; ABB66101.  
 XX  
 XX New isolated nucleic acid detection reagent for detecting 1000 or more  
 PT genes from Drosophila and for elucidating cell signalling and cell-cell  
 PT interactions -  
 XX  
 XX Claim 1; SEQ ID NO 25094; 21pp + Sequence Listing; English.  
 PS  
 XX  
 CC The invention relates to an isolated nucleic acid detection reagent  
 CC capable of detecting 1000 or more genes from Drosophila. The invention is  
 CC useful in developmental biology and in elucidating cell signalling and  
 CC cell-cell interactions in higher eukaryotes for the development of  
 CC insecticides, therapeutics and pharmaceutical drugs. The invention  
 CC discloses genomic DNA sequences (AB101840-AB116175), expressed DNA  
 CC sequences (AB101840-AB116175) and the encoded proteins  
 CC (AB57737-AB572072).  
 CC The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pcf\_sequences.  
 XX  
 SQ Sequence 3631 BP; 1115 A; 691 C; 711 G; 1114 T; 0 other;  
 Query Match 27.8%; Score 28.6; DB 23; Length 3631;  
 Best Local Similarity 59.0%; Pred. No. 21;  
 Matches 49; Conservative 0; Mismatches 34; Indels 0; Gaps 0;  
 QY 2 AAGTACGTGGAATACAGTTTAATGACAGCATTAATAGCTCCGATATGATTAATGCTA 61  
 DB 2172 AATGTTGGTATGTAACCTTTACAGTTTAATATTGCTGCTTAATATTAATATA 2113  
 QY 62 ATACAGTTAAAAAAGCGTATT 84  
 DB 2112 TTATAGTTAAATGACGGAATT 2090  
 RESULT 17  
 AAX82193  
 ID AAX82193 standard; DNA; 2341 BP.  
 XX  
 AC AAX82193;  
 XX  
 DT 18-AUG-1999 (first entry)  
 XX  
 XX Influenza virus PB1 protein gene sequence.  
 DE  
 XX Cold-adapted influenza virus; passage culture; PB2 protein; PB1 protein;  
 KW PA protein; NP protein; M protein; NS protein; temperature sensitivity;  
 KW vaccine; flu; influenza; ss.  
 KW  
 XX Influenza virus.  
 OS  
 PN WO9928445-A1.  
 XX  
 PD 10-JUN-1999.  
 XX  
 XX 30-NOV-1996; 98WO-KR00384.  
 PF  
 XX 29-NOV-1997; 97KR-0064854.  
 PR  
 XX (CHEI-) CHEIL JEDANG CORP.  
 PA  
 XX Cheoun KH, Kim HG, Kim J, Kim SJ, Lee KH, Seong BL;  
 PI Youn JW;  
 XX WPI; 1999-38537/32.  
 DR  
 XX Cold-adapted influenza viruses useful for the production of  
 PT protective vaccines against flu

XX Claim 4; Page 52-53; 62pp; English.

PS The invention relates to cold-adapted influenza viruses prepared by

XX passage culture of A/X-31, B/Yamagata/16/88 or B/Lee/40 viruses at low

CC temperatures. A cDNA gene of cold-adapted influenza virus H7CA-A101 can

CC be selected from a group consisting of PB2 protein gene, PB1 protein

CC gene, PA protein gene, NP protein gene, M protein gene and NS protein

CC gene (AA82192-x82197). The method is useful for the production of cold-

CC adapted influenza virus that exhibit temperature sensitivity and can be

CC actively grown in fertilized eggs. The virus is useful for vaccines for

CC protection against flu. Live vaccines containing cold-adapted viruses

CC have several advantages over killed vaccines. It can prevent reduction

CC of immunogenicity, which may occur in the killed vaccine where antigenic

CC proteins would be denatured at its inactivation. It can also avoid

CC hypersensitivity due to the prolonged administration of heterologous

CC proteins. It promotes the immunity by inducing iga and it can be

CC administered into a spray formulation via nasal cavity and thus its

CC application is convenient for children. It is able to inhibit the

CC growth of the wild-type virus and thus its therapeutic effect can be

CC expected. The present sequence represents the influenza virus PB1

CC protein gene.

CC

XX Sequence 2341 BP; 805 A; 461 C; 530 G; 545 T; 0 other;

SQ

Query Match 27.6%; Score 28.4; DB 20; Length 2341;

Best Local Similarity 56.4%; Pred. No. 22;

Matches 53; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

OY 10 GGAATACAGTTAATGACAGCATTAATAGCTCTGCATATGTAATGCTAATACAGTT 69

DB 2232 GAAGAAGAGTCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 2291

OY 70 AAAAAAAAAAGCTATTTCTTCCCTGCTCTGATCCACCA 103

DB 2292 AAAATAGTGAATTTAGCTGTCTTCATGAAAAA 2325

RESULT 18

AA235351

ID AA235351 standard; DNA; 41599 BP.

XX

AC AA235351;

XX

DT 27-MAR-2000 (first entry)

XX

DE Cosmid including sequence spanning human chromosome 9p21.

XX

KW Chromosome 9p21; human; cancer; tumour; diagnosis; prognosis;

KW methylthioadenosine phosphorylase; glioma; melanoma;

KW primary lymphoid malignancy; non-small cell lung cancer;

KW head and neck cancer; ovarian cancer; bladder cancer;

KW chondrosarcoma; ds.

XX

OS Homo sapiens.

XX

PN M09967634-A1.

XX

PD 29-DEC-1999.

XX

PF 21-JUN-1999; 99WC-US13981.

XX

PR 23-JUN-1998; 98US-0090411.

PR 17-JUN-1999; 99US-0335231.

XX

PA (REGC ) UNIV CALIFORNIA.

XX

PI Carson DA, Schmid M, Carrera CJ;

XX

DR WPI; 2000-126650/11.

XX

PT Diagnosing and determining prognosis for cancer causatively associated

PT with derangements of chromosome 9p21

XX Disclosure; Fig 7; 55pp; English.

PS This is the nucleotide sequence of a cosmid that includes sequences

XX spanning human chromosome 9p21 (ATCC AC00047). This region

CC harbours 5 genes within about 120 kb: the tumour suppressor genes

CC p16INK4A (p15) with its alternatively spliced form p10, p16INK4A

CC (p16) and p19ARF, and the gene for methylthioadenosine phosphorylase

CC (MTPAP). The invention provides a method for diagnosis of, and

CC determining a prognosis for, cancer causatively associated with

CC derangements of chromosome 9p21. Underlying the invention is the

CC discovery that such derangements have their geneis in deletions

CC occurring centromeric to STS 3.21, most often including breakpoints

CC in exon 8 and/or between exons 4 and 5 of the gene which encodes

CC MTPAP. As the cancer and tumour development advance, deletions in

CC 9p21 progress centromerically from the geneis point toward the

CC gene encoding p16. Thus, the method of the invention is performed

CC by determining whether (a) portions of the 9p21 region including

CC and telomeric to STS 3.21 are deleted, and (b) portions of the

CC 9p21 region centromeric to STS 3.21 are deleted, where a positive

CC finding in step (a) and a negative finding in step (b) are

CC indicative of a cancer in an early stage of tumour development

CC and a positive finding in step (a) is indicative of a cancer in an

CC advanced stage of tumour development. Primer pairs (see AA235354-75)

CC are provided for use in claimed methods for diagnosing and

CC determining a prognosis for cancer associated with derangements of

CC 9p21, especially a glioma, primary lymphoid malignancy, non-small

CC cell lung cancer, melanoma, head and neck cancer, ovarian cancer,

CC bladder cancer or a chondrosarcoma (claimed).

XX

SQ Sequence 41599 BP; 13477 A; 8216 C; 8242 G; 11664 T; 0 other;

Query Match 27.6%; Score 28.4; DB 21; Length 41599;

Best Local Similarity 58.1%; Pred. No. 38;

Matches 50; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

OY 5 TGACTGGAATACAGTTAATGACAGCATTAATAGCTCTGCATATGTAATGCTAATA 64

DB 5850 TAAATGAAAAAAGTTAATTAATGTTTCTCCCTGCAAACTTAAAAACACACA 5909

OY 65 CAGTTAAAAAAGCTATTTCTCCCTGG 90

DB 5910 CACATAAATCAGTGTCTTTCAGG 5935

RESULT 19

AAH08436

ID AAH08436 standard; CDNA; 804 BP.

XX

AC AAH08436;

XX

DT 26-JUN-2001 (first entry)

XX

DE Human cDNA clone (5'-primer) SEQ ID NO:5271.

XX

OS Human.

XX

PN Human, primer; detection; diagnosis; antisense therapy; gene therapy; ss.

XX

PD Homo sapiens.

XX

PF EPI074617-A2.

XX

PR 07-FEB-2001.

XX

PR 28-JUL-2000; 2000EP-0116126.

XX

PR 29-JUL-1999; 99JP-0248036.

PR 27-AUG-1999; 99JP-0300253.

PR 11-JAN-2000; 2000JP-0118776.

PR 02-MAY-2000; 2000JP-0183767.

PR 09-JUN-2000; 2000JP-0241899.

XX

PA (HELI-) HELIX RES INST.

PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;  
 PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;  
 XX  
 DR WPI: 2001-318749/34.  
 XX  
 PT Primer sets for synthesizing polynucleotides, particularly the 5602  
 PT full-length cDNAs defined in the specification, and for the detection  
 PT and/or diagnosis of the abnormality of the proteins encoded by the  
 PT full-length cDNAs -  
 XX  
 PS Claim 1: SEQ ID 5271: 2537pp + CD ROM; English.  
 XX  
 CC The present invention describes primer sets for synthesizing 5602  
 CC full-length cDNAs defined in the specification. Where a primer set  
 CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary  
 CC to the complementary strand of a polynucleotide which comprises one of  
 CC the 5602 nucleotide sequences defined in the specification, where the  
 CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination  
 CC of an oligonucleotide comprising a sequence complementary to the  
 CC complementary strand of a polynucleotide which comprises a 5'-end  
 CC sequence and an oligonucleotide comprising a sequence complementary to a  
 CC polynucleotide which comprises a 3'-end sequence, where the  
 CC oligonucleotide comprises at least 15 nucleotides and the combination of  
 CC the 5'-end sequence/3'-end sequence is selected from those defined in  
 CC the specification. The primer sets can be used in antisense therapy and  
 CC in gene therapy. The primers are useful for synthesizing polynucleotides,  
 CC particularly full-length cDNAs. The primers are also useful for the  
 CC detection and/or diagnosis of the abnormality of the proteins encoded by  
 CC the full-length cDNAs. The primers allow obtaining of the full-length  
 CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and  
 CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to  
 CC AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632  
 CC represent oligonucleotides, all of which are used in the exemplification  
 CC of the present invention.  
 CC  
 SQ Sequence 804 BP; 259 A; 170 C; 165 G; 207 T; 3 other;  
 XX  
 SO Query Match 27.4%; Score 28.2; DB 22; Length 804;  
 Best Local Similarity 61.6%; Pred. No. 21;  
 Matches 45; Conservative 0; Mismatches 28; Indels 0; Gaps 0;  
 OY 13 ATAACAGTTTAAAGCATTAATAGCTCGCATATGTGAATTCCTAATACAGTTAA 72  
 DB 424 ACAACCTTTTAAGATATCATTAACACACATCCCTTGGGAATTTGGAACCGGTTAA 483  
 OY 73 AAAACGGTATTTTC 85  
 DB 484 AGAGACACCTTTC 496  
 XX  
 RESULT 20  
 AAH18260  
 ID AAH18260 standard; cDNA: 2362 BP.  
 AC AAH18260;  
 XX  
 XX 26-JUN-2001 (first entry)  
 DT  
 XX Human cDNA sequence SEQ ID NO:18222.  
 DE  
 XX Human; primer: detection; diagnosis; antisense therapy; gene therapy; ss.  
 KM  
 XX Homo sapiens.  
 OS  
 XX  
 XX EP1074617-A2.  
 PN  
 XX 07-FEB-2001.  
 PD  
 XX 28-JUL-2000; 2000EP-0116126.  
 PF  
 XX 29-JUL-1999; 99JP-0248036.  
 PR 27-AUG-1999; 99JP-0300253.  
 PR 11-JAN-2000; 2000JP-0118776.

PR 02-MAY-2000; 2000JP-0183767.  
 PR 09-JUN-2000; 2000JP-0241899.  
 XX  
 XX (HELI-) HELIX RES INST.  
 PA  
 XX Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;  
 PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;  
 XX  
 DR WPI: 2001-318749/34.  
 XX  
 PT Primer sets for synthesizing polynucleotides, particularly the 5602  
 PT full-length cDNAs defined in the specification, and for the detection  
 PT and/or diagnosis of the abnormality of the proteins encoded by the  
 PT full-length cDNAs -  
 XX  
 PS Claim 8: SEQ ID 18222: 2537pp + CD ROM; English.  
 XX  
 CC The present invention describes primer sets for synthesizing 5602  
 CC full-length cDNAs defined in the specification. Where a primer set  
 CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary  
 CC to the complementary strand of a polynucleotide which comprises one of  
 CC the 5602 nucleotide sequences defined in the specification, where the  
 CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination  
 CC of an oligonucleotide comprising a sequence complementary to the  
 CC complementary strand of a polynucleotide which comprises a 5'-end  
 CC sequence and an oligonucleotide comprising a sequence complementary to a  
 CC polynucleotide which comprises a 3'-end sequence, where the  
 CC oligonucleotide comprises at least 15 nucleotides and the combination of  
 CC the 5'-end sequence/3'-end sequence is selected from those defined in  
 CC the specification. The primer sets can be used in antisense therapy and  
 CC in gene therapy. The primers are useful for synthesizing polynucleotides,  
 CC particularly full-length cDNAs. The primers are also useful for the  
 CC detection and/or diagnosis of the abnormality of the proteins encoded by  
 CC the full-length cDNAs. The primers allow obtaining of the full-length  
 CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and  
 CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to  
 CC AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632  
 CC represent oligonucleotides, all of which are used in the exemplification  
 CC of the present invention.  
 CC  
 SQ Sequence 2362 BP; 659 A; 512 C; 562 G; 629 T; 0 other;  
 XX  
 SO Query Match 27.4%; Score 28.2; DB 22; Length 2362;  
 Best Local Similarity 61.6%; Pred. No. 25;  
 Matches 45; Conservative 0; Mismatches 28; Indels 0; Gaps 0;  
 OY 13 ATAACAGTTTAAAGCATTAATAGCTCGCATATGTGAATTCCTAATACAGTTAA 72  
 DB 424 ACAACCTTTTAAGATATCATTAACACACATCCCTTGGGAATTTGGAACCGGTTAA 483  
 OY 73 AAAACGGTATTTTC 85  
 DB 484 AGAGACACCTTTC 496  
 XX  
 RESULT 21  
 AA243957  
 ID AA243957 standard; cDNA: 3002 BP.  
 AC AA243957;  
 XX  
 XX 17-MAR-2000 (first entry)  
 DT  
 XX Human DAN cDNA.  
 DE  
 XX  
 XX DAN; deadenylating nuclease; cytostatic; immunosuppressor; human;  
 KM neuroprotector; anti-inflammatory; cancer; autoimmune disease; ss.  
 XX  
 OS  
 XX Homo sapiens.  
 XX  
 XX Key Location/Qualifiers  
 FT CDS 58..1977  
 FT /\*tag= a

FT XX /product= "DAN"  
PN MO9958647-A2.  
XX  
PD 18-NOV-1999.  
XX  
PF 05-MAY-1999: 99WO-EP03071.  
XX  
PR 08-MAY-1998: 98DE-1022122.  
XX  
PA (AVERT ) AVENTIS RES & TECHNOLOGIES GMBH & CO KG.  
XX  
PI Huels C, Gallert K, Koerner C, Wahle E;  
XX WPI: 2000-072335/06.  
DR  
XX DNA encoding a human deadenylation nuclease, used to, e.g. treat  
PT Alzheimer's disease -  
XX  
PS Claim 3: Page 39-40; 46pp; German.  
XX  
CC This invention describes a novel nucleic acid (I) encoding a human  
CC deadenylation nuclease (DAN) which has cytostatic, immunosuppressive,  
CC neuroprotective and anti-inflammatory activity. (I) can be used to  
CC identify functional interactors, to identify and isolate human variants  
CC from Genbank or to treat or diagnose cancer, autoimmune disease, in  
CC particular multiple sclerosis or rheumatoid arthritis, Alzheimer's  
CC disease, allergies, especially neurodermatitis, Type I or IV allergies,  
CC arthrosis, atherosclerosis, osteoporosis, acute and chronic infections  
CC and/or diabetes and/or influencing cell metabolism, in particular  
CC immunosuppression for transplantation. This sequence encodes a human DAN  
CC protein which is described in the method of the invention.  
XX  
SQ Sequence 3002 BP; 869 A; 633 C; 703 G; 797 T; 0 other;  
XX  
Query Match 27.4%; Score 28.2; DB 21; Length 3002;  
Best Local Similarity 61.6%; Pred. No. 27;  
Matches 45; Conservative 0; Mismatches 28; Indels 0; Gaps 0;  
OY 13 ATACAGCTTTAATGACAGCATTAATAGCTCCGATATGTAATGCTAATACAGTTAA 72  
DB 1050 ACAACCTTTTAAGGATATCATTAACAACATCCCTTGCGAATGTGAAACGCGTTAAA 1109  
OY 73 AAACGCTATTTC 85  
DB 1110 ACAGACACCTTTC 1122  
XX  
RESULT 22  
ACCA6483  
ID ACC64683 standard; cDNA; 3073 BP.  
XX  
AC ACC64683;  
XX  
DT 02-JUN-2003 (first entry)  
XX  
DE Human dlthp nucleic acid synthesis/modification protein-encoding cDNA.  
XX  
KW Human: dlthp; diagnostic and therapeutic polynucleotide; diagnosis;  
KW cancer; cell proliferative disorder; autoimmune disorder;  
KW inflammatory disorder; infection; hormonal disorder; metabolic disorder;  
KW neurological disorder; gastrointestinal disorder; transport disorder;  
KW connective tissue disorder; drug screening; proteome analysis;  
KW gene therapy; antisense therapy; genotyping; transgenic animal; knock in;  
KW disease model; toxicological testing; transcript imaging;  
KW nucleic acid synthesis; nucleic acid modification; gene; ss.  
XX  
OS Homo sapiens.  
XX  
PN MO200297031-A2.  
XX  
PD 05-DEC-2002.  
XX

PF 27-MAR-2002; 2002WO-US10056.  
XX  
PR 28-MAR-2001; 2001US-279619P.  
XX  
PR 29-MAR-2001; 2001US-280067P.  
XX  
PR 29-MAR-2001; 2001US-280068P.  
XX  
PR 16-MAY-2001; 2001US-291280P.  
XX  
PR 17-MAY-2001; 2001US-291829P.  
XX  
PR 17-MAY-2001; 2001US-291849P.  
XX  
PR 19-JUN-2001; 2001US-299428P.  
XX  
PR 20-JUN-2001; 2001US-299776P.  
XX  
PR 20-JUN-2001; 2001US-300001P.  
XX  
PA (INCYTE) INCYTE GENOMICS INC.  
XX  
XX  
PI Daffo A, Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J;  
PI Dufour GE, Hillman JL, Yu JY, Tason O, Yap PE, Amshay SR;  
PI Daugherty SC, Dam TC, Liu TF, Nguyen DA, Kleefeld Y, Gerstlin EH;  
PI Peralta CH, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B;  
PI Flores V, Marwaha R, Lo A, Lan RV, Urashka ME;  
XX  
XX WPI: 2003-129518/12.  
DR  
DR P-PSDB; ABR41545.  
XX  
XX Novel human diagnostic and therapeutic polypeptide useful for  
PT identifying test compound which specifically binds to a polypeptide  
PT encoded by human diagnostic and therapeutic polynucleotide, and to  
PT induce antibodies -  
XX  
PS Claim 2; SEQ ID No 404; 591pp; English.  
XX  
CC The invention relates to novel human diagnostic and therapeutic  
CC polynucleotides designated dlthp (ACC64680-ACC646749) and to their  
CC encoded proteins (DTRP; ABR41136-ABR41812). The invention also relates  
CC to polynucleotide sequences at least 90% identical to the dlthp cDNA  
CC sequences of the invention; recombinant vectors, host cells and  
CC transgenic organisms comprising a dlthp nucleic acid sequence; the  
CC recombinant production of DTRP proteins; antibodies specific for DTRP  
CC proteins; microarrays comprising dlthp nucleic acid sequences; methods  
CC of detecting dlthp nucleotide and protein sequences; methods of screening  
CC for compounds which specifically bind a DTRP protein; and methods of  
CC assessing the toxicity of test compounds using a dlthp hybridisation  
CC probe. Dthp nucleic acid sequences and DTRP proteins may be used in the  
CC diagnosis of a wide variety of conditions including cancer and other cell  
CC proliferative disorders; autoimmune or inflammatory disorders; bacterial,  
CC viral, fungal or parasitic infections; hormonal disorders; metabolic  
CC disorders; neurological disorders; gastrointestinal disorders; transport  
CC disorders; and connective tissue disorders. They may also be used to  
CC screen for modulators of protein activity or gene expression. DTRP  
CC proteins can additionally be used in analysis of the proteome of a tissue  
CC or cell type and to induce antibodies. The dlthp nucleic acids are  
CC additionally useful in somatic or germline gene therapy of the disorders  
CC mentioned above, as a source of antisense sequences, as a source of  
CC probes and primers, in genotyping and identification of individuals, in  
CC the generation of transgenic animal models of human disease or knock in  
CC humanised animals, in toxicological testing, and in transcript imaging.  
CC The present sequence represents a dlthp cDNA encoding a DTRP protein  
CC which is involved in nucleic acid synthesis and/or modification.  
CC Note: The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 3073 BP; 861 A; 662 C; 735 G; 815 T; 0 other;  
XX  
Query Match 27.4%; Score 28.2; DB 25; Length 3073;  
Best Local Similarity 61.6%; Pred. No. 27;  
Matches 45; Conservative 0; Mismatches 28; Indels 0; Gaps 0;  
OY 13 ATACAGCTTTAATGACAGCATTAATAGCTCCGATATGTAATGCTAATACAGTTAA 72  
DB 1133 ACAACCTTTTAAGGATATCATTAACAACATCCCTTGCGAATGTGAAACGCGTTAAA 1192  
OY 73 AAACGCTATTTC 85  
XX

Db 1193 AGAGACACCTTC 1205

RESULT 23  
AAK51618  
ID AAK51618 standard; cDNA; 3078 BP.

XX AAK51618;  
AC AAK51618;  
XX  
XX  
XX 06-NOV-2001 (first entry)  
XX  
XX Human polynucleotide SEQ ID NO 163.  
XX  
XX  
XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;  
XX vaccine; peptide therapy; stem cell growth factor; haematopoiesis;  
XX tissue growth factor; immunomodulatory; cancer; leukaemia;  
XX nervous system disorder; arthritis; inflammation; ss.  
XX  
XX Homo sapiens.  
XX WO200157190-A2.  
XX  
XX  
XX 09-AUG-2001.  
XX  
XX  
XX 05-FEB-2001; 2001WO-US04098.  
XX  
XX  
XX 03-FEB-2000; 2000US-0496914.  
XX 27-APR-2000; 2000US-0560875.  
XX 20-JUN-2000; 2000US-0598075.  
XX 19-JUL-2000; 2000US-0620325.  
XX 01-SEP-2000; 2000US-0654936.  
XX 15-SEP-2000; 2000US-0663561.  
XX 20-OCT-2000; 2000US-0693325.  
XX 30-NOV-2000; 2000US-0728422.  
XX  
XX  
XX (HYSE-) HYSEQ INC.  
XX  
XX Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;  
XX Zhao Qa, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;  
XX Xue AJ, Yang Y, Wejhrman T, Goodrich R;  
XX  
XX WPI: 2001-476283/51.  
XX P-PSDB: AAM78485.  
XX  
XX Nucleic acids encoding polypeptides with cytokine-like activities,  
XX useful in diagnosis and gene therapy -  
XX  
XX  
XX Claim 1; Page 886-889; 6221pp; English.  
XX  
XX The invention relates to polynucleotides (AAK51456-AAK53435) and the  
XX encoded polypeptides (AAM78323-AAW80302) that exhibit activity elating to  
XX cytokine, cell proliferation or cell differentiation or which may induce  
XX production of other cytokines in other cell populations. The  
XX polynucleotides and polypeptides are useful in gene therapy, vaccines or  
XX peptide therapy. The polypeptides have various cytokine-like activities,  
XX e.g. stem cell growth factor activity, haematopoiesis regulating  
XX activity, tissue growth factor activity, immunomodulatory activity and  
XX activin/inhibin activity and may be useful in the diagnosis and/or  
XX treatment of cancer, leukaemia, nervous system disorders, arthritis and  
XX inflammation.  
XX Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666  
XX (AAM80020) are omitted as the relevant pages from the sequence listing  
XX were missing at the time of publication.  
XX  
XX Sequence 3078 BP; 873 A; 664 C; 729 G; 812 T; 0 other;

Query Match 27.4%; Score 28.2; DB 22; Length 3078;  
Best Local Similarity 61.6%; Pred. No. 27;  
Matches 45; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

OY 13 ATACAGTTTAATGACAGATTAAAGCTCTGCATATGTAATGCTCAATACAGTTAAA 72  
Db 1133 ACAACCTTTAAGATATCAATTAACAACATCCCTGCGAATTGGAAGGCGGTTAAA 1192

OY 73 AAACGGTATTC 85  
ID AAK52602  
Db 1193 AGAGACACCTTC 1205

RESULT 24  
AAK52602  
ID AAK52602 standard; cDNA; 3086 BP.

XX AAK52602;  
AC AAK52602;  
XX  
XX  
XX 06-NOV-2001 (first entry)  
XX  
XX Human polynucleotide SEQ ID NO 2131.  
XX  
XX  
XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;  
XX vaccine; peptide therapy; stem cell growth factor; haematopoiesis;  
XX tissue growth factor; immunomodulatory; cancer; leukaemia;  
XX nervous system disorder; arthritis; inflammation; ss.  
XX  
XX Homo sapiens.  
XX WO200157190-A2.  
XX  
XX  
XX 09-AUG-2001.  
XX  
XX  
XX 05-FEB-2001; 2001WO-US04098.  
XX  
XX  
XX 03-FEB-2000; 2000US-0496914.  
XX 27-APR-2000; 2000US-0560875.  
XX 20-JUN-2000; 2000US-0598075.  
XX 19-JUL-2000; 2000US-0620325.  
XX 01-SEP-2000; 2000US-0654936.  
XX 15-SEP-2000; 2000US-0663561.  
XX 20-OCT-2000; 2000US-0693325.  
XX 30-NOV-2000; 2000US-0728422.  
XX  
XX  
XX (HYSE-) HYSEQ INC.  
XX  
XX Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;  
XX Zhao Qa, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;  
XX Xue AJ, Yang Y, Wejhrman T, Goodrich R;  
XX  
XX WPI: 2001-476283/51.  
XX P-PSDB: AAM79469.  
XX  
XX Nucleic acids encoding polypeptides with cytokine-like activities,  
XX useful in diagnosis and gene therapy -  
XX  
XX  
XX Claim 1; Page 4503-4504; 6221pp; English.  
XX  
XX The invention relates to polynucleotides (AAK51456-AAK53435) and the  
XX encoded polypeptides (AAM78323-AAW80302) that exhibit activity elating to  
XX cytokine, cell proliferation or cell differentiation or which may induce  
XX production of other cytokines in other cell populations. The  
XX polynucleotides and polypeptides are useful in gene therapy, vaccines or  
XX peptide therapy. The polypeptides have various cytokine-like activities,  
XX e.g. stem cell growth factor activity, haematopoiesis regulating  
XX activity, tissue growth factor activity, immunomodulatory activity and  
XX activin/inhibin activity and may be useful in the diagnosis and/or  
XX treatment of cancer, leukaemia, nervous system disorders, arthritis and  
XX inflammation.  
XX Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666  
XX (AAM80020) are omitted as the relevant pages from the sequence listing  
XX were missing at the time of publication.  
XX  
XX Sequence 3086 BP; 873 A; 668 C; 729 G; 815 T; 1 other;

Query Match 27.4%; Score 28.2; DB 22; Length 3086;  
Best Local Similarity 61.6%; Pred. No. 27;  
Matches 45; Conservative 0; Mismatches 28; Indels 0; Gaps 0;



PR 18-AUG-1998; 98US-0096950.  
PR 18-AUG-1998; 98US-0096959.  
PR 18-AUG-1998; 98US-0096960.  
PR 18-AUG-1998; 98US-0097022.  
PR 19-AUG-1998; 98US-0097141.  
PR 20-AUG-1998; 98US-0097218.  
PR 24-AUG-1998; 98US-0097661.  
PR 26-AUG-1998; 98US-0097951.  
PR 26-AUG-1998; 98US-0097952.  
PR 26-AUG-1998; 98US-0097954.  
PR 26-AUG-1998; 98US-0097955.  
PR 26-AUG-1998; 98US-0097971.  
PR 26-AUG-1998; 98US-0097974.  
PR 26-AUG-1998; 98US-0097978.  
PR 26-AUG-1998; 98US-0097979.  
PR 26-AUG-1998; 98US-0097986.  
PR 26-AUG-1998; 98US-0098014.  
PR 31-AUG-1998; 98US-0098525.  
PR 16-SEP-1998; 98US-0100634.  
PR 12-JAN-1999; 99US-0115565.  
XX  
XX (GETH ) GENENTECH INC.  
XX  
PI Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;  
PI Wood WI, Yuan J;  
XX  
XX WPI: 2000-072883/06.  
XX  
XX Membrane-bound proteins and related nucleotide sequences -  
XX  
XX Examples: Fig 60; 822pp; English.  
XX  
XX The invention provides membrane-bound PRO polypeptides and  
CC polynucleotides encoding them. The PRO sequences of the invention were  
CC identified based on extracellular domain homology screening. The PRO  
CC sequences have homology with proteins including LDL receptors, TIE  
CC ligands and various enzymes. The membrane-bound proteins and receptor  
CC molecules are useful as pharmaceutical and diagnostic agents. Receptor  
CC immunoadhesins, for instance, can be used as therapeutic agents to block  
CC receptor-ligand interactions. The membrane-bound proteins can also be  
CC employed for screening of potential peptide or small molecule inhibitors  
CC of the relevant receptor/ligand interaction. The PRO encoding sequences  
CC are useful as hybridization probes, in chromosome and gene mapping and in  
CC the generation of antisense RNA and DNA. PRO nucleic acid sequences  
CC will also be useful for the preparation of PRO polypeptides, especially  
CC by recombinant techniques.  
XX  
XX Sequence 466 BP; 116 A; 77 C; 115 G; 149 T; 9 other:  
XX  
XX Query Match 27.2%; Score 28; DB 21; Length 466;  
XX Best Local Similarity 59.7%; Pred. No. 21;  
XX Matches 46; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

KW cell death; cancer; chromosomal mapping; gene mapping; tissue typing;  
KW diagnostic assay; ss.  
XX  
XX Homo sapiens.  
OS  
XX WO200073454-A1.  
XX  
XX  
XX 07-DEC-2000.  
XX  
XX 30-MAR-2000; 2000WO-US08439.  
XX  
XX 02-JUN-1999; 99WO-US12252.  
XX 23-JUN-1999; 99US-0141037.  
XX 07-JUL-1999; 99US-0143048.  
XX 20-JUL-1999; 99US-0144758.  
XX 26-JUL-1999; 99US-0145698.  
XX 28-JUL-1999; 99US-0146222.  
XX 17-AUG-1999; 99US-0149396.  
XX 15-SEP-1999; 99WO-US21090.  
XX 15-SEP-1999; 99WO-US21547.  
XX 08-OCT-1999; 99US-0158663.  
XX 30-NOV-1999; 99WO-US28313.  
XX 01-DEC-1999; 99WO-US28301.  
XX 16-DEC-1999; 99WO-US30095.  
XX 20-DEC-1999; 99WO-US30911.  
XX 05-JAN-2000; 2000WO-US00219.  
XX 06-JAN-2000; 2000WO-US00376.  
XX 11-FEB-2000; 2000WO-US03565.  
XX 18-FEB-2000; 2000WO-US04341.  
XX 22-FEB-2000; 2000WO-US04414.  
XX 24-FEB-2000; 2000WO-US04914.  
XX 24-FEB-2000; 2000WO-US05004.  
XX 02-MAR-2000; 2000WO-US05841.  
XX 15-MAR-2000; 2000WO-US06884.  
XX 20-MAR-2000; 2000WO-US07377.  
XX  
XX (GETH ) GENENTECH INC.  
XX  
XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;  
XX Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski RJ;  
XX Grimaldi CJ, Gurney AL, Kijavyn IJ, Napier MA, Pan J, Peoni NF;  
XX Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;  
XX Zhang Z;  
XX  
XX WPI: 2001-032160/04.  
XX  
XX PRO polynucleotides used to produce polypeptides used to target  
PT bioactive molecules such as toxins, radiolabels or antibodies, to  
PT specific cells, to cause targeted cell death -  
XX  
XX Example 25; Fig 60; 935pp; English.  
XX  
XX The present invention describes human secreted and transmembrane PRO  
CC proteins. The PRO proteins have cytostatic activity. The PRO proteins  
CC can be used for targeted delivery of bioactive molecules, such as  
CC toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide  
CC sequences, and their fragments, can be used as hybridisation probes, in  
CC chromosomal and gene mapping, and in the generation of anti-sense RNA  
CC and DNA. They may also be used to produce transgenic animals which are  
CC used to develop and screen therapeutically useful reagents. The PRO  
CC nucleotide and protein sequence can be used for tissue typing and in  
CC treating cancer. Anti-PRO antibodies can be used in diagnostic assays.  
CC AAF44270 to AAF44470 represent PCR primers and hybridisation probes used  
CC in the isolation of human PRO sequences. AAF44087 to AAF44269 and  
CC AAB65154 to AAB65300 represent human PRO polynucleotide and protein  
CC sequences given in the exemplification of the present invention.  
XX  
XX Sequence 466 BP; 116 A; 77 C; 115 G; 149 T; 9 other:  
XX  
XX Query Match 27.2%; Score 28; DB 22; Length 466;  
XX Best Local Similarity 59.7%; Pred. No. 21;  
XX Matches 46; Conservative 0; Mismatches 31; Indels 0; Gaps 0;



QY 5 TGACTGGAATACAGTTTAATGACAGATTATAGTCCTCCATATGTAATGCTTATA 64  
||| ||| | ||| ||| | ||| ||| ||| ||| | | |  
Db 216 TGAGTGTGTTAAATCTTTCATGCGGATAAATACAGCTGATCATATGATATCCACA 157  
QY 65 CAGTTAAAAAACGGTA 81  
| | ||||| |||  
Db 156 CCTGTAAAAAATAGTA 140

RESULT 27  
ABX80189/c  
ID ABX80189 standard; DNA; 466 BP.  
XX  
AC ABX80189;  
XX  
DT 28-APR-2003 (first entry)  
XX  
De Novel human secreted or transmembrane protein related DNA28357.  
XX  
KW Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;  
KW cardiac insufficiency disorder; cancer; tumour; immune response;  
KW adrenal cortical capillary endothelial growth; c-fos induction;  
KW vascular endothelial growth factor inhibition; VEGF inhibition;  
KW endothelial cell growth inhibitor; T-lymphocytes stimulation;  
KW retinal neurons cell survival; rod photoreceptor cell survival;  
KW retinal disorder; retinitis pigmentosa; kidney disorder;  
KW mammalian kidney mesangial cell proliferation; Berger disease;  
KW dermatitis; herpesiformis; Crohn's disease; chondrocyte differentiation;  
KW chondrocyte redifferentiation; sports injury; arthritis; gene; ds.  
XX  
OS Homo sapiens.  
XX  
PN US2002132252-A1.  
XX  
PD 19-SEP-2002.  
XX  
PF 14-NOV-2001; 2001US-0990442.  
XX  
PR 05-NOV-1997; 97WO-US20069.  
PR 16-SEP-1998; 98WO-US19330.  
PR 17-SEP-1998; 98WO-US19437.  
PR 07-OCT-1998; 98WO-US21141.  
PR 01-DEC-1998; 98WO-US25108.  
PR 05-JAN-1999; 99WO-US00106.  
PR 08-MAR-1999; 99WO-US05028.  
PR 02-JUN-1999; 99WO-US12252.  
PR 15-SEP-1999; 99WO-US21090.  
PR 15-SEP-1999; 99WO-US21547.  
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PR 01-DEC-1999; 99WO-US28634.  
PR 16-DEC-1999; 99WO-US30095.  
PR 20-DEC-1999; 99WO-US30911.  
PR 06-JAN-2000; 2000WO-US00219.  
PR 06-JAN-2000; 2000WO-US00376.  
PR 11-FEB-2000; 2000WO-US03565.  
PR 18-FEB-2000; 2000WO-US04341.  
PR 22-FEB-2000; 2000WO-US04414.  
PR 24-FEB-2000; 2000WO-US04914.  
PR 02-MAR-2000; 2000WO-US05004.  
PR 10-MAR-2000; 2000WO-US05841.  
PR 15-MAR-2000; 2000WO-US06319.  
PR 20-MAR-2000; 2000WO-US06884.  
PR 30-MAR-2000; 2000WO-US07377.  
PR 15-MAY-2000; 2000WO-US08439.  
PR 17-MAY-2000; 2000WO-US13358.  
PR 22-MAY-2000; 2000WO-US13705.  
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PR 23-AUG-2000; 2000WO-US22031.  
PR

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PR 28-FEB-2001; 2001WO-US06520.  
PR 01-JUN-2001; 2001WO-US17800.  
PR 20-JUN-2001; 2001WO-US19692.  
PR 29-JUN-2001; 2001WO-US21066.  
PR 09-JUL-2001; 2001WO-US21735.  
PR 16-JUN-1997; 97US-0478787.  
PR 17-OCT-1997; 97US-0622508.  
PR 12-NOV-1997; 97US-0651866.  
PR 13-NOV-1997; 97US-0653116.  
PR 24-NOV-1997; 97US-0667709.  
PR 25-FEB-1998; 98US-0759459.  
PR 20-MAR-1998; 98US-0789106.  
PR 28-APR-1998; 98US-0833226.  
PR 07-MAY-1998; 98US-0846006.  
PR 28-MAY-1998; 98US-0871066.  
PR 02-JUN-1998; 98US-0876076.  
PR 02-JUN-1998; 98US-0877599.  
PR 03-JUN-1998; 98US-0878276.  
PR 04-JUN-1998; 98US-0880216.  
PR 04-JUN-1998; 98US-0880256.  
PR 04-JUN-1998; 98US-0880266.  
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PR 04-JUN-1998; 98US-0880306.  
PR 04-JUN-1998; 98US-0880336.  
PR 04-JUN-1998; 98US-0883266.  
PR 05-JUN-1998; 98US-0881676.  
PR 05-JUN-1998; 98US-0882026.  
PR 05-JUN-1998; 98US-0882126.  
PR 05-JUN-1998; 98US-0882176.  
PR 09-JUN-1998; 98US-0886556.  
PR 10-JUN-1998; 98US-0887346.  
PR 10-JUN-1998; 98US-0887386.  
PR 10-JUN-1998; 98US-0887426.  
PR 10-JUN-1998; 98US-0888106.  
PR 10-JUN-1998; 98US-0888246.  
PR 10-JUN-1998; 98US-0888266.  
PR 11-JUN-1998; 98US-0888586.  
PR 11-JUN-1998; 98US-0888616.  
PR 11-JUN-1998; 98US-0888766.  
PR 12-JUN-1998; 98US-0891056.  
PR 16-JUN-1998; 98US-0894406.  
PR 16-JUN-1998; 98US-0895126.  
PR 16-JUN-1998; 98US-0895146.  
PR 17-JUN-1998; 98US-0895326.  
PR 17-JUN-1998; 98US-0895386.  
PR 17-JUN-1998; 98US-0895986.  
PR 17-JUN-1998; 98US-0895996.  
PR 17-JUN-1998; 98US-0896006.  
PR 17-JUN-1998; 98US-0896536.  
PR 18-JUN-1998; 98US-0898016.  
PR 18-JUN-1998; 98US-0898076.  
PR 18-JUN-1998; 98US-0899086.  
PR 28-AUG-2001; 2001US-0941992.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL,  
PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ,  
PI Grimaldi JC, Gurney AL, Kijavlin IJ, Napier MA, Pan J, Paoni NF,  
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI,  
PI Zhang Z;  
XX  
DR WPI, 2003-247083/24.  
XX  
PT Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346  
PT and PRO1375, which stimulate proliferation of stimulated T-lymphocytes  
PT are therapeutically useful for enhancing immune response and in cancer  
PT treatments





xx PR 05-NOV-1997; 97WO-US20069.  
PR 16-SEP-1998; 98WO-US19330.  
PR 17-SEP-1998; 98WO-US19437.  
PR 07-OCT-1998; 98WO-US21141.  
PR 01-DEC-1998; 98WO-US25108.  
PR 05-JAN-1999; 99WO-US00106.  
PR 08-MAR-1999; 99WO-US05028.  
PR 02-JUN-1999; 99WO-US12252.  
PR 15-SEP-1999; 99WO-US21547.  
PR 30-NOV-1999; 99WO-US28313.  
PR 01-DEC-1999; 99WO-US28301.  
PR 01-DEC-1999; 99WO-US28634.  
PR 16-DEC-1999; 99WO-US30095.  
PR 20-DEC-1999; 99WO-US30911.  
PR 05-JAN-2000; 2000WO-US00219.  
PR 06-JAN-2000; 2000WO-US00376.  
PR 11-FEB-2000; 2000WO-US03565.  
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PR 22-FEB-2000; 2000WO-US04414.  
PR 24-FEB-2000; 2000WO-US04914.  
PR 02-MAR-2000; 2000WO-US05004.  
PR 10-MAR-2000; 2000WO-US05841.  
PR 15-MAR-2000; 2000WO-US06319.  
PR 20-MAR-2000; 2000WO-US06884.  
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PR 15-MAY-2000; 2000WO-US08439.  
PR 17-MAY-2000; 2000WO-US13358.  
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PR 23-AUG-2000; 2000WO-US23522.  
PR 24-AUG-2000; 2000WO-US23328.  
PR 08-NOV-2000; 2000WO-US30952.  
PR 01-DEC-2000; 2000WO-US32678.  
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PR 12-NOV-1997; 97US-065186P.  
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PR 24-NOV-1997; 97US-066770P.  
PR 25-FEB-1998; 98US-075945P.  
PR 20-MAR-1998; 98US-078910P.  
PR 28-APR-1998; 98US-083322P.  
PR 07-MAY-1998; 98US-084600P.  
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PR 04-JUN-1998; 98US-087827P.  
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PR 02-JUL-1998; 98US-091673P.  
PR 07-JUL-1998; 98US-091978P.  
PR 09-JUL-1998; 98US-092182P.  
PR 10-JUL-1998; 98US-092472P.  
PR 20-JUL-1998; 98US-093339P.  
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PR 04-AUG-1998; 98US-095285P.  
PR 04-AUG-1998; 98US-095301P.  
PR 04-AUG-1998; 98US-095302P.  
PR 04-AUG-1998; 98US-095318P.  
PR 04-AUG-1998; 98US-095321P.  
PR 04-AUG-1998; 98US-095325P.  
PR 10-AUG-1998; 98US-095916P.  
PR 10-AUG-1998; 98US-095929P.  
PR 10-AUG-1998; 98US-096012P.  
PR 11-AUG-1998; 98US-096143P.  
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PR 17-AUG-1998; 98US-096773P.  
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PR 17-AUG-1998; 98US-096895P.  
PR 17-AUG-1998; 98US-096897P.  
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PR 18-AUG-1998; 98US-096954P.  
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PR 19-AUG-1998; 98US-097141P.  
PR 20-AUG-1998; 98US-097218P.  
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PR 26-AUG-1998; 98US-097971P.  
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PR 26-AUG-1998; 98US-097986P.  
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Query Match 27.28; Score 28; DB 25; Length 466;  
Best Local Similarity 59.78; Pred. No. 21;  
Matches 46; Conservatively 0; Mismatches 31; Indels 0; Gaps 0;

QY 5 TGACTGGAATACGTTTATGACATTAATACCTCCCTCATATGTGAATTCCTAATA 64  
DB 216 TGAGTGGTTNAATCTTTGATGCTGATTAATACAGCTGCATCTATGATTAATCCACA 157  
QY 65 CAGCTAAAAAACGGTA 81  
DB 156 CCCTGTAATAAATAGTA 140

## RESULT 30

ABX90166/c

ID ABX90166 standard; cDNA; 466 BP.

AC ABX90166;

XX 01-MAY-2003 (first entry)

XX Human secreted/transmembrane protein cDNA, #38.

KW Human; gene; ss; PRO; secreted; transmembrane; signal peptide;

KW pharmaceutical; diagnostic; therapeutic; gene therapy.

XX Homo sapiens.

OS US2002160384-A1.

XX US2002160384-A1.

XX 31-OCT-2002.

XX 14-NOV-2001; 2001US-0992598.

XX 05-NOV-1997; 97WO-US20069.

XX 16-SEP-1998; 98WO-US19330.

XX 17-SEP-1998; 98WO-US19437.

XX 07-OCT-1998; 98WO-US21141.

XX 01-DEC-1998; 98WO-US25108.

XX 05-JAN-1999; 99WO-US00106.

XX 08-MAR-1999; 99WO-US05028.

XX 02-JUN-1999; 99WO-US12252.

XX 15-SEP-1999; 99WO-US21090.

XX 15-SEP-1999; 99WO-US21547.

PR 30-NOV-1999; 99WO-US28313.  
PR 01-DEC-1999; 99WO-US28301.  
PR 01-DEC-1999; 99WO-US28634.  
PR 16-DEC-1999; 99WO-US30095.  
PR 20-DEC-1999; 99WO-US30911.  
PR 05-JAN-2000; 2000WO-US00219.  
PR 06-JAN-2000; 2000WO-US00376.  
PR 11-FEB-2000; 2000WO-US03565.  
PR 18-FEB-2000; 2000WO-US04341.  
PR 22-FEB-2000; 2000WO-US04414.  
PR 24-FEB-2000; 2000WO-US04914.  
PR 24-FEB-2000; 2000WO-US05004.  
PR 02-MAR-2000; 2000WO-US05841.  
PR 10-MAR-2000; 2000WO-US06319.  
PR 15-MAR-2000; 2000WO-US06884.  
PR 20-MAR-2000; 2000WO-US07377.  
PR 30-MAR-2000; 2000WO-US08439.  
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PR 11-AUG-2000; 2000WO-US22031.  
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PR 01-DEC-2000; 2000WO-US32678.  
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PR 07-MAY-1998; 98US-084600P.  
PR 28-MAY-1998; 98US-087106P.  
PR 02-JUN-1998; 98US-087607P.  
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PR 03-JUN-1998; 98US-087827P.  
PR 04-JUN-1998; 98US-088021P.  
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PR 04-JUN-1998; 98US-088028P.  
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PR 05-JUN-1998; 98US-088167P.  
PR 05-JUN-1998; 98US-088202P.  
PR 05-JUN-1998; 98US-088212P.  
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PR 09-JUN-1998; 98US-088655P.  
PR 10-JUN-1998; 98US-088734P.  
PR 10-JUN-1998; 98US-088738P.  
PR 10-JUN-1998; 98US-088742P.  
PR 10-JUN-1998; 98US-088810P.  
PR 10-JUN-1998; 98US-088824P.  
PR 10-JUN-1998; 98US-088826P.  
PR 11-JUN-1998; 98US-088858P.  
PR 11-JUN-1998; 98US-088861P.  
PR 11-JUN-1998; 98US-088876P.  
PR 12-JUN-1998; 98US-089105P.  
PR 16-JUN-1998; 98US-089440P.  
PR 16-JUN-1998; 98US-089512P.  
PR 16-JUN-1998; 98US-089514P.

PR 17-JUN-1998: 98US-089532P.  
PR 17-JUN-1998: 98US-089538P.  
PR 17-JUN-1998: 98US-089558P.  
PR 17-JUN-1998: 98US-089599P.  
PR 17-JUN-1998: 98US-089600P.  
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PR 18-JUN-1998: 98US-089907P.  
PR 18-JUN-1998: 98US-089908P.  
PR 28-AUG-2001: 2001US-0941992.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;  
PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;  
PI Grimaldi JC, Gurney AL, Kijavlin IJ, Napier MA, Pan J, Paoni NF;  
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;  
PI Zhang Z;  
XX  
DR WPI: 2003-288106/28.  
XX  
PT New transmembrane polypeptides and nucleic acids encoding the  
PT polypeptides, useful in gene therapy, in chromosome identification, as  
PT chromosome markers, or in generating probes -  
XX  
PS Example 25: Fig 60; 650pp; English.  
XX  
CC The invention discloses isolated PRO secreted/transmembrane polypeptides  
CC comprising a sequence without signal peptide and the nucleic acid  
CC encoding them. The polypeptides can be used to raise antibodies that  
CC specifically bind to the PRO polypeptide, for linking a bioactive  
CC molecule to a cell expressing a PRO protein and for modulating at least  
CC one biological activity of a cell. The PRO polypeptides or  
CC polynucleotides are also useful in gene therapy, in chromosome  
CC identification, as chromosome markers, or in generating probes. The PRO  
CC polypeptides are useful as molecular markers for protein  
CC electrophoresis, and the isolated nucleic acids may be used for  
CC recombinantly expressing those markers. The PRO polypeptides and nucleic  
CC acids may also be used in tissue typing. Anti-PRO antibodies are useful  
CC in diagnostic assays for PRO, and in affinity purification of PRO from  
CC recombinant cell culture or natural sources. The sequences presented in  
CC ABX90083-ABX90468 are the genes encoding, the primers amplifying and the  
CC probes detecting the PRO polynucleotides of the invention.  
CC Note: The sequence data for this patent is also available in electronic  
CC format from USPTO at [seqdata.uspto.gov/sequence.html](http://seqdata.uspto.gov/sequence.html).  
XX  
SQ Sequence 466 BP; 116 A; 77 C; 115 G; 149 T; 9 other;  
XX  
Query Match 27.2%; Score 28; DB 25; Length 466;  
Best Local Similarity 59.7%; Pred. No. 21;  
Matches 46; Conservative 0; Mismatches 31; Indels 0; Gaps 0;  
OY 5 TGACGTGCAATACAGTTCATTAATAGCTCCTCGATATGATTCGTAATA 64  
DB 216 TCGAGTGCTTNAATCTTCATCATGTGGATTAATACAGCTCATATATCAACCA 157  
OY 65 CAGTTAAAAAAGGTA 81  
DB 156 CCGTGTAAAAAATAGTA 140  
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RESULT 31  
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ID ABX77777 standard; CDNA; 466 BP.  
XX  
AC ABX77777;  
XX  
DT 14-APR-2003 (first entry)  
XX  
DE Human PRO polynucleotide #163.  
XX  
KW Human: PRO; gene; ss; cytosolic; tumour; cancer; breast; lung; stomach;  
KW liver; horse; cow; dog; cat; sheep; pig; goat; rabbit; ADEPT;  
KW

KW antibody-dependent enzyme mediated prodrug therapy.  
OS Homo sapiens.  
XX  
PN US2003027163-A1.  
XX  
PD 06-FEB-2003.  
XX  
PE 15-NOV-2001; 2001US-0997666.  
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PR 05-NOV-1997: 97WO-US20069.  
PR 16-SEP-1998: 98WO-US19330.  
PR 17-SEP-1998: 98WO-US19437.  
PR 07-OCT-1998: 98WO-US21141.  
PR 01-DEC-1998: 98WO-US25108.  
PR 05-JAN-1999: 99WO-US00106.  
PR 08-MAR-1999: 99WO-US05028.  
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Best Local Similarity 59.7%; Pred. No. 21;
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RESULT 32.
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ID ABX79373 standard; cDNA: 466 BP.
AC ABX79373;
XX 17-APR-2003 (first entry)
XX Human secreted/transmembrane protein cDNA, #38.
DE Human; gene; ss: PRO; secreted; transmembrane; signal peptide;
KW pharmaceutical; diagnostic; biosensor; bioreactor; tumour; therapeutic;
KW colon cancer; lung cancer; breast cancer; cancer; gene therapy.
XX Homo sapiens.
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XX  03-OCT-2002.
XX
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XX  05-NOV-1997; 97WO-US20069.
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PR  18-JUN-1998; 98US-089907P.
PR  18-JUN-1998; 98US-089908P.
PR  28-AUG-2001; 2001US-0941992.

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(GETH ) GENENTECH INC.

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XX  Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DJ,
PI  Ferrara N, Fong S, Gether H, Gerritsen ME, Goddard A, Godowski PJ,
PI  Grimaldi JC, Gurney AL, Kijavlin IJ, Napier MA, Pan J, Paoni NF,
PI  Roy MA, Stewart TA, Tamas D, Watanabe CK, Williams PM, Wood WI,
PI  Zhang Z;
XX

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WPI; 2003-155950/15.

New secreted and transmembrane PRO polypeptides (e.g. PRO183, PRO184, PRO361 or PRO846) useful as targets for therapeutic intervention in cancers (e.g. lung or breast cancers), or for diagnosing these cancers

Example 25; Fig 60; 647pp; English.

The invention discloses isolated PRO secreted/transmembrane polypeptides comprising a sequence without signal peptide and the nucleic acid encoding them. The polypeptides can be used to raise antibodies that specifically bind to the PRO polypeptide, for linking a bioactive molecule to a cell expressing a PRO protein and for modulating at least one biological activity of a cell. The PRO polypeptides or polynucleotides are also useful as pharmaceuticals, diagnostics, biosensors or bioreactors, for detecting or treating e.g. tumours in mammals, e.g. humans, dogs, cats, cattle, horses, sheep, pigs or rabbits as targets for therapeutic intervention in certain cancers (e.g. colon, lung or breast cancers) and diagnostic determination of the presence of these cancers. The PRO polypeptides are also useful as molecular weight markers or for chromosome identification. The PRO genes are useful as hybridisation probes or for screening libraries of human cDNA, genomic DNA or mRNA. The PRO genes may also be used in gene therapy, particularly for replacing a defective gene. The sequences presented in ABX79290-ABX79675 are the genes encoding, the primers amplifying and the probes detecting the PRO polynucleotides of the invention.

CC Note: The sequence data for this patent is also available in electronic format from USPTO at [seqdata.uspto.gov/sequence.html](http://seqdata.uspto.gov/sequence.html).

CC Sequence 466 BP; 116 A; 77 C; 115 G; 149 T; 9 other;

XX Query Match 27.2%; Score 28; DB 25; Length 466;  
Best Local Similarity 59.7%; Pred. No. 21;  
Matches 46; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

OY 5 TGACGTGGAATACAGCTTAATGACAGCACTTAATAGCTCTCTGCATATGTGCAATTGCTAATA 64



CC polypeptides, and for identifying agonists or antagonists.  
CC The polynucleotide sequences encoding PRO polypeptides are useful as  
CC hybridisation probes, in chromosome and gene mapping, in the generation  
CC of antisense RNA and DNA, in the preparation of PRO polypeptides, for  
CC generating transgenic animals or knockout animals, to construct  
CC hybridisation probes for mapping the gene which encodes the PRO  
CC polypeptide, and for the genetic analysis of individuals with genetic  
CC disorders, in gene therapy, for chromosome identification, as  
CC chromosome markers, and for generating probes for PCR, Northern  
CC analysis, Southern analysis and Western analysis. The present  
CC sequence represents a human PRO cDNA clone.  
CC Note: The sequence data for this patent was obtained in electronic  
CC format directly from the USPTO web site at  
CC [seqdata.uspto.gov/psipsidentry.html](http://seqdata.uspto.gov/psipsidentry.html).  
CC  
XX  
SQ Sequence 466 BP; 116 A; 77 C; 115 G; 149 T; 9 other;  
  
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Best Local Similarity 59.7%; Pred No. 21;  
Matches 46; Conservative 0; Mismatches 31; Indels 0; Gaps 0;  
  
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ID ABX16976 standard; cDNA; 466 BP.  
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XX ABX16976;  
XX  
DT 04-FEB-2003 (first entry)  
XX  
DE Human PRO polynucleotide #163.  
XX  
XX Human; PRO; gene; ss; secreted polypeptide; transmembrane polypeptide;  
KW toxin; radiolabel; cell death; gene mapping; chromosome mapping;  
KW protein electrophoresis; genetic disorder; immunosuppressive; cytostatic;  
antibacterial.  
XX  
OS Homo sapiens.  
XX  
PN US2002123463-A1.  
XX  
PD 05-SEP-2002.  
XX  
PF 19-NOV-2001; 2001US-0989732.  
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PR 18-JUN-1998; 98US-089801P.  
PR 18-JUN-1998; 98US-089907P.  
PR 18-JUN-1998; 98US-089908P.  
PR 28-AUG-2001; 2001US-0941992.

XX (GENENTECH INC.  
 PA Ashkenazi AJ, Baker KP, Botstein D, Desnovers L, Eaton DL,  
 XX Ferrera N, Fong S, Geider H, Gerritsen ME, Goddard A, Godowski PJ,  
 PI Grimaldi JC, Gurey AL, Kijaviri IU, Napier MA, Pan J, Paoi NF,  
 PI Roy MA, Stewart TA, Tamas D, Watanabe CK, Williams PM, Wood WI,  
 PI Zhang Z;  
 DR WPI: 2003-066810/06.  
 XX  
 PT Novel secreted and transmembrane polypeptide for modulating biological  
 PT activity of cell expressing the polypeptide, identifying agonists or  
 PT antagonists of polypeptide, and as molecular weight markers  
 XX  
 PS Disclosure: Fig 60: 655pp; English.  
 XX  
 CC The invention relates to a secreted and transmembrane polypeptide, termed  
 CC PRO polypeptide, and the polynucleotide encoding it. The polypeptide is  
 CC useful for detecting PRO polypeptides and for linking a bioactive  
 CC molecule to a cell expressing the above polypeptides, where the bioactive  
 CC molecule is a toxin, radiolabel or an antibody. The bioactive material  
 CC causes the death of the cell. The polypeptide is useful for identifying  
 CC agonists or antagonists of the PRO polypeptide, for preparing variants of  
 CC PRO, as a molecular weight marker for protein electrophoresis purposes  
 CC and the PRO polynucleotide is useful for recombinantly expressing those  
 CC markers. The polynucleotide is also useful as a hybridisation probe, in  
 CC chromosome and gene mapping, in generation of antisense RNA and DNA, in  
 CC the preparation of PRO polypeptide, for generating transgenic animals or  
 CC knockout animals which in turn are useful in the development and  
 CC screening of therapeutically useful reagents, to construct hybridisation  
 CC probes for mapping the gene which encodes PRO and for the genetic  
 CC analysis of individuals with genetic disorders, in gene therapy, for  
 CC chromosome identification, as a chromosome marker and for generating  
 CC probes for PCR, Northern analysis, Southern analysis and Western  
 CC analysis. This sequence represents a human PRO polynucleotide of the  
 CC invention.  
 CC  
 SO Sequence 466 BP; 116 A; 77 C; 115 G; 149 T; 9 other;  
 XX  
 Query Match 27.2%; Score 28; DB 25; Length 466;  
 Best Local Similarity: 59.7%; Pred. No. 21;  
 Matches 46; Conservative 0; Mismatches 31; Indels 0; Gaps 0;  
 OY 5 TGACGATTAACAGTTAATGACACGATTAATAGCTCTGCTATGTAATGCTAATA 64  
 DB 216 TGAGTGTGTTAAATCTTCAATGCTGATTAACACGCTCATGATTAATCCACCA 157  
 OY 65 CAGTTAAAAAAGCGTA 81  
 DB 156 CCTGTAAAAAATAGTA 140  
 XX  
 RESULT 35  
 ABS76828/c  
 ID ABS76828 standard; cDNA: 725 BP.  
 XX  
 AC ABS76828;  
 XX  
 DT 12-DEC-2002 (first entry)  
 XX  
 DE Frog embryonic gene sequence Q9925237 #1.  
 XX  
 KW Frog; ss; embryonic development; developmental disorder;  
 KW microarray; cell differentiation.  
 XX  
 OS Xenopus laevis.  
 XX  
 OS US2002081610-A1.  
 XX  
 PN 27-JUN-2002.  
 PD  
 PF 23-JUL-2001; 2001US-0910943.  
 XX  
 PF

XX 21-JUL-2000; 2000US-219658P.  
 PR  
 XX (UYRQ ) UNIV ROCKEFELLER.  
 PA  
 XX Hemmati-Briyanlou A, Altman CR;  
 PI WPI: 2002-626534/67.  
 DR  
 XX  
 PT Nucleic acid array containing Xenopus embryonic nucleic acids is useful  
 PT to identify genes involved in embryonic development, to identify  
 PT different types of embryonic cells, and to diagnose developmental  
 PT disorders  
 XX  
 PS Claim 1; Page 98; 823pp; English.  
 XX  
 CC The invention relates to a nucleic acid array, where each coordinate  
 CC contains a single nucleic acid species having one of 770 nucleotide  
 CC sequences (appearing as ABS76747-ABS77516) a of a Xenopus embryonic gene  
 CC product, or its complement or hybridisable fragment of not less than  
 CC 20 contiguous nucleotides of one of those sequences. Also included are  
 CC detecting differential expression of embryonic genes, comprising:  
 CC (a) contacting a nucleic acid array comprising genes expressed in  
 CC embryonic but not mature cells with nucleic acids from sample and  
 CC control cells; and (b) detecting differential hybridisation of nucleic  
 CC acids from the sample cells relative to the control cells; and detecting  
 CC defects in development, comprising: (a) contacting nucleic acids from  
 CC test cells undergoing development with a nucleic acid array of gene  
 CC products known to play a fundamental role in the development process; and  
 CC (b) detecting a difference in expression of a fundamental gene in the  
 CC sample cells relative to a standard. The invention is useful to identify  
 CC genes involved in embryonic development and related processes such as  
 CC cell differentiation. This would be useful for diagnosing developmental  
 CC disorders and for identifying different types of embryonic cells.  
 CC The present sequence is one of the 770 Xenopus embryonic cDNA sequences.  
 CC  
 SO Sequence 725 BP; 215 A; 137 C; 165 G; 206 T; 2 other;  
 XX  
 Query Match 27.2%; Score 28; DB 24; Length 725;  
 Best Local Similarity 58.3%; Pred. No. 23;  
 Matches 49; Conservative 0; Mismatches 35; Indels 0; Gaps 0;  
 OY 9 TCGAATTAACAGTTAATGACAGCATTATAGCTTCGATATGTAATGCTAATACAGT 68  
 DB 664 TGTGATTTCTTTTAAGTGGCAATTGTATATCTTGTTCTGTGCTTCCGATTAACAGT 605  
 OY 69 TAAAAAAGCGTATTTCCCTGCTT 92  
 DB 604 TTGACCAATGATATTTGCTTCTT 581  
 XX  
 RESULT 36  
 ABS76832/c  
 ID ABS76832 standard; cDNA: 725 BP.  
 XX  
 AC ABS76832;  
 XX  
 DT 12-DEC-2002 (first entry)  
 XX  
 DE Frog embryonic gene sequence Q9925237 #2.  
 XX  
 KW Frog; ss; embryonic development; developmental disorder;  
 KW microarray; cell differentiation.  
 XX  
 OS Xenopus laevis.  
 XX  
 OS US2002081610-A1.  
 XX  
 PN 27-JUN-2002.  
 PD  
 PF 23-JUL-2001; 2001US-0910943.  
 XX  
 PF 21-JUL-2000; 2000US-219658P.  
 XX



CC	AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
CC	amino acid sequences given in AAM82170 to AAM91921. (I) have cytosolic
CC	activity, and can be used in gene therapy and vaccine production. (I)
CC	proteins and polynucleotides may be used in the prevention, diagnosis and
CC	treatment of diseases associated with inappropriate (I) expression. For
CC	example, they may be used to treat disorders associated with decreased
CC	expression by rectifying mutations or deletions in a patient's genome
CC	that affect the activity of (I) by expressing inactive proteins or to
CC	supplement the patients own production of (I). Additionally, (I)
CC	polynucleotides may be used to produce the secreted (I), by inserting
CC	the nucleic acids into a host cell and culturing the cell to express the
CC	protein. (I) proteins and polynucleotides may be used to prevent,
CC	diagnose and treat immune/haematopoietic-related diseases, especially
CC	cancers and cancer metastases of haematopoietic-derived cells. AAK64703
CC	to AAK87694 represent human immune/haematopoietic antigen genomic
CC	sequences from the present invention. AAK54942 to AAK54950 and AAM82169
CC	represent sequences used in the exemplification of the present invention.
CC	
XX	Sequence 378 BP; 125 A; 60 C; 71 G; 117 T; 5 other;
SQ	
Query Match	27.0%; Score 27.8; DB 22; Length 378;
Best Local Similarity	56.6%; Pred. No. 24;
Matches	47; Conservative 2; Mismatches 34; Indels 0; Gaps 0;
QY	19. GTTTAATGACAGCATTTATAGCTCTCGCATATGTGAATTGCTAATACAGTTAAAAAAGC 78
Db	9 GGTTCCTTAACAGATTTAATAATATCAACCCAGTCATTAAATTTTAAAAAGACTTTAAATAT 68
QY	79 GTATTTCCCTGGTTCTGATCCAA 101
Db	69 GTGTTTCATTATTAAGGAAACAA 91
RESULT 38	
AAK81718/c	
ID	AAK81718 standard; DNA; 2024 BP.
XX	
AC	AAK81718;
XX	
DT	26-FEB-2001 (first entry)
XX	
DE	Human secreted protein coding sequence SEQ ID NO: 19.
XX	
KW	Cytostatic; immunosuppressive; neutropic; neuroprotective; antiviral;
KW	antiallergic; hepatotropic; antididiabetic; antiinflammatory; antifurc;
KW	vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic;
KW	cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
KW	neurological disease; infection; human; secreted protein; ss.
XX	
OS	Homo sapiens.
XX	
FN	WO200061627-A1.
XX	
PD	19-OCT-2000.
XX	
PE	06-APR-2000; 2000WO-US09067.
XX	
PR	09-APR-1999; 99US-0128697.
XX	
PR	20-JAN-2000; 2000US-0176929.
XX	
PA	(HUMA-) HUMAN GENOME SCI INC.
XX	(ROSE/) ROSEN C A.
PI	Rosen CA, Ruben SM, Komatsoulis G;
XX	
DR	WPI; 2000-647419/62.
XX	
DR	P-PSDB; AAB45394.
XX	
FT	New nucleic acid molecules encoding 49 human secreted proteins for
XX	diagnosing, preventing, treating or ameliorating medical conditions and
XX	used as food additives or preservatives -







OY 73 AAACGTAATTCCTGCTGTTCTGATCCAC 102  
 DB 2316 AGAAGATATGATCTGACTGAATATTAAC 2345

## RESULT 43

ABV47128  
 ID ABV47128 standard; cDNA; 444 BP.

AC ABV47128;

DT 16-SEP-2002 (first entry)

DE Human prostate expression marker cDNA 47119.

KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;  
 KM pharmacogenomic marker; gene; ss.

OS Homo sapiens.

PN WO200160860-A2.

PD 23-AUG-2001.

PF 20-FEB-2001; 2001WO-US05171.

PR 17-FEB-2000; 2000US-183319P.

PR 16-MAR-2000; 2000US-189862P.

PR 25-MAY-2000; 2000US-207454P.

PR 09-JUN-2000; 2000US-211314P.

PR 18-JUL-2000; 2000US-219007P.

PR 13-DEC-2000; 2000US-255281P.

PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

PI Schlegel R, Endege WO, Monahan JE;

PS WPI: 2001-662795/76.

XX Novel isolated nucleic acid molecule associated with cancerous state of

CC prostate cells and correlating with presence of prostate cancer, useful

CC for detecting presence of prostate cancer, stage of prostate cancer -

XX Claim 1; Page 9277; 11750pp; English.

CC The invention relates to an isolated nucleic acid molecule (I) comprising

CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the

CC specification or its complement. (I) is useful for:

CC (a) assessing whether a patient is afflicted with prostate cancer;

CC (b) monitoring the progression of prostate cancer in a patient;

CC (c) assessing the efficacy of a test compound to inhibit prostate

CC cancer in a patient;

CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer

CC in a patient;

CC (e) selecting a composition for inhibiting prostate cancer in a patient;

CC (f) assessing the prostate cell carcinogenic potential of a compound;

CC (g) determining whether prostate cancer has metastasized in a patient;

CC (h) assessing the aggressiveness or indolence of prostate cancer in a

CC patient;

CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.

XX Sequence 444 BP; 129 A; 107 C; 71 G; 137 T; 0 other;

SO Query Match 26.6%; Score 27.4; DB 23; Length 444;

Best Local Similarity 55.9%; Pred. No. 33;

Matches 52; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

OY 9 TGGAAATACAGTTTATATACAGATTATAGCTCTGATATGATGCTAATACAGT 68

DB 151 TGAATATGCTATCCATGCTTACATGATGATTTATTTCAAAATTTGTTGTAATAAGT 210

OY 69 TAAAAAAGGATTTCCCTGTTCTGATCCA 101

DB 211 TTGAAAAACATTTATATTTTGTAAATTTCCA 243

## RESULT 44

AB241332  
 ID AB241332 standard; DNA; 588 BP.

AC AB241332;

DT 07-MAR-2003 (first entry)

DE N. gonorrhoeae nucleotide sequence SEQ ID 7253.

KW Antibacterial; infection; vaccine; gene therapy; gene; ds.

OS Neisseria gonorrhoeae.

PN WO200279243-A2.

PD 10-OCT-2002.

PF 12-FEB-2002; 2002WO-IB02069.

PR 12-FEB-2001; 2001GB-0003424.

PA (CHIR-) CHIRON SPA.

PI Fontana MR, Pizsa M, Masianni V, Monaci E;

PR WPI: 2003-058415/05.

DR P-PSDB; ABP80362.

PT New protein from Neisseria gonorrhoeae, useful for the manufacture of a

PT medicament for treating or preventing N. gonorrhoeae infection -

PS Disclosure; Page 715; 815pp; English.

XX The present invention relates to proteins from Neisseria gonorrhoeae.

CC Also disclosed are the nucleic acid molecules encoding the proteins and

CC antibodies that specifically bind to the proteins. The composition

CC comprising the protein, nucleic acid or antibody is useful for the

CC manufacture of a medicament for treating or preventing N. gonorrhoeae

CC infection, this may be in the form of a vaccine or gene therapy.

CC Sequences given in records AB237706-AB242016 represent nucleic acid

CC molecules of the invention.

XX Sequence 588 BP; 186 A; 112 C; 122 G; 168 T; 0 other;

SO Query Match 26.6%; Score 27.4; DB 25; Length 588;

Best Local Similarity 65.6%; Pred. No. 35;

Matches 40; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

OY 25 TCACAGCAATTAATAGCTCTGATATGATGATGCTAATGCTAATGCTAATTT 84

DB 287 TGTACCACTAAATAATTCCTGTAATGCTAATTTAAATACCGTAAACACCAATTTT 346

OY 85 C 85

DB 347 C 347

RESULT 45

AB241770

ID AB241770 standard; DNA; 588 BP.

AC AB241770;

DT 07-MAR-2003 (first entry)

DE N. gonorrhoeae nucleotide sequence SEQ ID 8129.

KW Antibacterial; infection; vaccine; gene therapy; gene; ds.

```

XX  Neisseria gonorrhoeae.
OS
XX  WO200279243-A2.
PN
XX  10-OCT-2002.
PD
XX  12-FEB-2002; 2002WO-1B02069.
PF
XX  12-FEB-2001; 2001GB-0003424.
PR
XX  (CHIR-) CHIRON SPA.
PA
XX  Fontana MR, Pizsa M, Massignani V, Monaci E;
PI
XX  WPI; 2003-058415/05.
DR
XX  P-PSDB; ABP80800.
PT
XX  New protein from Neisseria gonorrhoeae, useful for the manufacture of a
PS  medicament for treating or preventing N. gonorrhoeae infection -
XX  Disclosure; Page 781; 815pp; English.
XX
CC  The present invention relates to proteins from Neisseria gonorrhoeae.
CC  Also disclosed are the nucleic acid molecules encoding the proteins and
CC  antibodies that specifically bind to the proteins. The composition
CC  comprising the protein, nucleic acid or antibody is useful for the
CC  manufacture of a medicament for treating or preventing N. gonorrhoeae
CC  infection, this may be in the form of a vaccine or gene therapy.
CC  Sequences given in records AB237706-AB242016 represent nucleic acid
CC  molecules of the invention.
XX
SQ  Sequence 588 BP; 186 A; 112 C; 122 G; 168 T; 0 other;
XX
Query Match      26.6%; Score 27.4; DB 25; Length 588;
Best Local Similarity 65.6%; Pred. No. 35;
Matches 40; Conservative 0; Mismatches 21; Indels 0; Gaps 0;
OY  25 TGACAGCATTAATAGCTCCTGCATATGTAATGCTAATACAGTTAAAAACGGTATTT 84
DB  287 TGTACAACTAAATAATTCCTGTAATGTGTATTTAAATAACGTAATAAACACCATTTT 346
OY  85 C 85
DB  347 C 347

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 Job time : 181 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 25, 2003, 06:47:22 ; Search time 1595 Seconds

(without alignments)  
2641.813 Million cell updates/sec

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Scoring table: IDENTITY\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 2888711 seqs, 2045481386 residues

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Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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2: gb.htg:\*  
3: gb.in:\*  
4: gb.om:\*  
5: gb.ov:\*  
6: gb.pat:\*  
7: gb.ph:\*  
8: gb.pl:\*  
9: gb.pr:\*  
10: gb.ro:\*  
11: gb.sts:\*  
12: gb.sy:\*  
13: gb.un:\*  
14: gb.vi:\*  
15: em.ba:\*  
16: em.fun:\*  
17: em.hum:\*  
18: em.in:\*  
19: em.mu:\*  
20: em.om:\*  
21: em.ov:\*  
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25: em.ro:\*  
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29: em.vl:\*  
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32: em.htg.other:\*  
33: em.htg.mus:\*  
34: em.htg.pla:\*  
35: em.htg.rtd:\*  
36: em.htg.mam:\*  
37: em.htg.vrl:\*  
38: em.sy:\*  
39: em.htgo.hum:\*  
40: em.htgo.mus:\*  
41: em.htgo.other:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	55.2	53.6	12793	9 AFI93556	AFI93556 Homo sapi
3	55.2	53.6	92693	9 AL157766	AL157766 Human DNA
4	55.2	53.6	99819	2 AC079761	AC079761 Homo sapi
5	53.6	52.0	11492	6 AX119933	AX119933 Sequence
6	53.6	52.0	11493	10 AFI93557	AFI93557 Mus muscu
7	53.6	52.0	283096	2 AC138718	AC138718 Mus muscu
8	49	47.6	722	11 BV018667	BV018667 S212P6240
9	48.8	47.4	240277	2 AC126559	AC126559 Rattus no
10	37.6	36.5	92309	2 AC021908	AC021908 Homo sapi
11	36.2	35.1	74962	6 AR253940	AR253940 Sequence
12	36.2	35.1	74962	6 AX350371	AX350371 Sequence
13	36.2	35.1	190648	9 CNS01DX1	AL139317 Human chr
14	34.4	33.4	291738	2 AC097744	AC097744 Mus muscu
15	33.8	32.8	156547	10 AC117262	AL928639 Mouse DNA
16	33.8	32.8	177843	10 AL928639	AL928639 Mus muscu
17	33.8	32.8	248044	2 BX284649	BX284649 Mus muscu
18	33.2	32.2	172022	2 AC134425	AC134425 Mus muscu
19	33.2	32.2	180219	9 AC099520	AC099520 Homo sapi
20	33.2	32.2	205222	2 AC130698	AC130698 Mus muscu
21	32.8	31.8	554	11 BV000942	BV000942 S209P6376
22	32.8	31.8	40033	9 HS1110P6	AL049175 Human DNA
23	32.6	31.7	156493	2 AC141553	AC141553 Rattus no
24	32.6	31.7	209701	2 AC111966	AC111966 Rattus no
25	32.6	31.7	252839	2 AC095096	AC095096 Rattus no
26	32.6	31.7	256498	2 AC118378	AC118378 Rattus no
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31	32.4	31.5	198176	2 AC069127	AC069127 Homo sapi
32	32.4	31.5	205394	2 AL954337	AL954337 Danio rer
33	32.4	31.5	207756	2 AC021546	AC021546 Homo sapi
34	32.4	31.5	57810	2 AC125433	AC125433 Homo sapi
35	32	31.1	95616	9 AC104655	AC104655 Homo sapi
36	32	31.1	132120	9 AC026733	AC026733 Homo sapi
37	32	31.1	137331	2 AC015774	AC015774 Homo sapi
38	32	31.1	172387	2 AC103561	AC103561 Homo sapi
39	32	31.1	191682	2 AC062005	AC062005 Homo sapi
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41	31.8	30.9	248948	2 AC097421	AC097421 Rattus no
42	31.6	30.7	1604	6 AX702602	AX702602 Sequence
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44	31.6	30.7	110000	2 AC112392.2	Continuation (3 of
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#### ALIGNMENTS

RESULT 1  
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LOCUS AX119931 12793 bp DNA linear PAT 11-MAY-2001  
DEFINITION Sequence 1 from Patent WO0129266.  
ACCESSION AX119931  
VERSION AX119931.1 GI:14036678  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1  
AUTHORS Hudson,T.J., Engert,J. and Richter,A.  
TITLE Identification of arsacs mutations and methods of use therefor  
JOURNAL Patent: WO 0129266-A 1 26-APR-2001;

FEATURES  
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QY 1 GAAGTACTGGAATAACAGTTTAATGACAGCATTAATAGCTCCTGCATATGTAATTGCT 60  
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 DB 6543 GAAGTACTGGAATAACAGTTTAATGACAGCATTAATAGCTCCTGCATATGTAATTGCT 6602  
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QY 61 AATAAGTTAAAAAAGCTATTTCCTGCTT 92  
 |||||

DB 6603 TAATACAGTTAAAAAAGCTATTTCCTGCTT 6634

RESULT 2  
 AF193556 12793 bp DNA linear PRI 07-FEB-2000  
 LOCUS  
 DEFINITION Homo sapiens saccin (SACS) gene, complete cds.  
 ACCESSION AF193556  
 VERSION AF193556.1 GI:6907041  
 KEYWORDS  
 SOURCE  
 ORGANISM Homo sapiens (human)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 1 (bases 1 to 12793)  
 Engert,J.C., Berube,P., Mercier,J., Dore,C., Lepage,P., Ge,B.,  
 Bouchard,J.P., Mathieu,J., Melancon,S.B., Schalling,M.,  
 Lander,E.S., Morgan,K., Hudson,T.J. and Richter,A.  
 ARSACS, a spastic ataxia common in northeastern Quebec, is caused  
 by mutations in a new gene encoding an 11.5-kb ORF  
 Nat. Genet. 24 (2), 120-125 (2000)

TITLE  
 10655055  
 2 (bases 1 to 12793)  
 Engert,J.C., Berube,P., Dore,C., Lepage,P., Ge,B., Hudson,T.J. and  
 Richter,A.  
 Direct Submission  
 Submitted (08-OCT-1999) Genome Centre, Montreal General Hospital,  
 1650 Cedar Ave., Montreal, QC H3G 1A4, Canada

JOURNAL  
 PUBMED  
 JOURNAL

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 TDSSEKRIIOELAIKFRINSHDOGSSTKLGCKVLIHTHTAKLPADLRISIVD  
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BASE COUNT  
 4163 a 2256 c 2487 g 3887 t

ORIGIN

Query Match  
 Best Local Similarity 75.0%; Pred No. 2.4e-05;  
 Matches 69; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 1 GAAGTACTGGAATAACAGTTTAATGACAGCATTAATAGCTCCTGCATATGTAATTGCT 60  
 |||||  
 DB 6543 GAAGTACTGGAATAACAGTTTAATGACAGCATTAATAGCTCCTGCATATGTAATTGCT 6602  
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QY 61 AATAAGTTAAAAAAGCTATTTCCTGCTT 92

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Db 6603 TAATACAGTTAAAAACGATATTCCTGCT 6634

RESULT 3  
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LOCUS  
DEFINITION Human DNA sequence from clone RP11-40020 on chromosome 11q12.11-12.2, complete sequence.  
ACCESSION AL157766  
VERSION AL157766  
KEYWORDS GI:13620292  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eulhemia; Primates; Catarrhini; Hominidae; Homo.  
AUTHORS Tromans, A.  
TITLE Direct Submission  
JOURNAL Submitted (11-APR-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk  
COMMENT  
Requests: clonerequest@sanger.ac.uk  
On Apr 12, 2001 this sequence version replaced gi:12709868.  
During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.  
This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em, EMBL; SW, SWISSPROT; Tr, TrEMBL; Wp, WORMPEP; Information on the WORMPEP database can be found at  
http://www.sanger.ac.uk/Projects/C\_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 13, constructed by the Sanger Centre Chromosome 13 Mapping Group. Further information can be found at  
http://www.sanger.ac.uk/HGP/Chr13  
RP11-40020 is from the library RPCT-11.1 constructed by the group of Pieter de Jong. For further details see  
http://www.chori.org/Dacpac/home.htm  
VECTOR: pBACE3.6  
IMPORTANT: This sequence is not the entire insert of clone RP11-40020. It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap.  
The true left end of clone RP11-760M1 is at 92594 in this sequence. The true right end of clone RP11-72P19 is at 100 in this sequence.  
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DEFINITION	Homo sapiens chromosome UNK clone RP11-14317, *** SEQUENCING IN			
	PROGRESS *** 44 unordered pieces.			
ACCESSION	AC079761			
VERSION	AC079761.1	GI:10047966		
KEYWORDS	HTG; HTGS_PHASE1.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Cranialta; Vertebrata; Euteleostomi;			
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
	1 (bases 1 to 99819)			
REFERENCE	Waterston, R.H.			
AUTHORS	The sequence of Homo sapiens clone			
TITLE	Unpublished			
JOURNAL	2 (bases 1 to 99819)			
REFERENCE	Waterston, R.H.			
AUTHORS	Direct Submission			
TITLE	Submitted (10-SEP-2000) Genome Sequencing Center, Washington			
JOURNAL				

**COMMENT**

Submitted (10-SEP-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA

Center: Washington University Genome Sequencing Center  
Web site: <http://genome.wustl.edu/gsc/index.shtml>  
----- Project Information -----

Project Information

```

* NOTE: This is a 'working draft' sequence. It currently
* consists of 44 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

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QY      61  AATACAGTTAATAAAGCGTATTTCCTCGTGT 92
DB      86892 TAAATACAGTTAATAAAGCGTATTTCCTCGTGT 86861

RESULT 5
AX119933
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LOCUS AX119933 11492 bp DNA linear PAT 11-MAY-2001  
DEFINITION Sequence 3 from Patent WO0129266.  
ACCESSION AX119933  
VERSION AX119933.1 GI:14036679  
KEYWORDS  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE  
1 Hudson, T.J., Engert, J. and Richter, A.  
Identification of araspas mutations and methods of use therefor  
Patent: WO 0129266-A 3 26-APR-2001;  
MCGILL UNIVERSITY (CA); Hopital Sainte-Justine (CA)  
FEATURES  
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Best Local Similarity 73.9%; Pred. No. 6.9e-05;  
Matches 68; Conservative 0; Mismatches 24; Indels 0; Gaps 0;  
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DB 6466 GAAGTACTGGAATTAATGATTAATGACGACATTAATGACCTGATGTTGAGTTAC 6525  
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DB 6526 TAATCAGTTAAAAAAGCGTATTTCCCTGCT 6557  
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LOCUS AF193557  
DEFINITION Mus musculus sacsin gene, complete cds.  
ACCESSION AF193557  
VERSION AF193557.1 GI:6907043  
KEYWORDS  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE  
1 (bases 1 to 11493)  
Engert, J.C., Berube, P., Mercier, J., Dore, C., Lepage, P., Ge, B.,  
Bouchard, J.P., Mathieu, J., Melancon, S.B., Schalling, M.,  
Lander, E.S., Morgan, K., Hudson, T.J. and Richter, A.  
ARSAKs, a spastic ataxia common in northeastern Quebec, is caused  
by mutations in a new gene encoding an 11.5-kb ORF  
Nat. Genet. 24 (2), 120-125 (2000)  
TITLE  
JOURNAL  
MEDLINE  
PUBMED  
10655055  
2 (bases 1 to 11493)  
Engert, J.C., Berube, P., Dore, C., Lepage, P., Ge, B., Hudson, T.J. and  
Richter, A.  
Direct Submission  
Submitted (08-OCT-1999) Genome Centre, Montreal General Hospital,  
1650 Cedar Ave., Montreal, QC H3G 1A4, Canada  
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TPSEKERKIIQETLEKRIHNSDGGISSTYKCKCKKXIDHTAKLPDRLASVYD  
SSDEATRLAMKLEKLTTSCLFVLDIGAFYTOEEVTOIMLIMENSLANE  
NSVLDLIMPLKFIHMSQGVAAADLPEDIPEDILEVLENEEACFPPTIFTSPTIL  
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OSSEGMALKKIKWYPACKERPNGPSVMMGDJCNLCAPDMCAHVALVEGSLP  
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MHDSLSEKDSFKALKPVMWTKNCPNLAQVITRPHLDIOPYLXNPKMKRPHO  
LRKAGSITELTSDHSIYQKYIYKSDDELESEBSKQHLMLIMRLYNOIPAS  
PNTPVYHSRNPSSKLVMKPHECCCDIKYDNDLLEDSVEPILIVHEDIPMKTAE  
WLVPLCLSTRINPEMMGEGSGOREPLVIRKNIIEPVSVDIFELKLRADANANA  
TECSFMIDRRMNDIRENLDGMAACHGPALENSSEFSDPFLNTRLESKRG  
EVDKVGKFGELGFSNVYHTIDPIINSRREMIENDPINISIKRDSRPGIKINXK  
OOKRLKPNOKRPPTDVRGCOLPLAVEPYVYNTPLPSTRIOEAKVSSVSCY  
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NPSFLGKTIQIDIGSEKIVSSDLVYFSRDESSQNRKDSAPTPYTSIPTEKLPGLR  
SILPLESGEKESHKSPSTRKHSRKLKVALPEILKEVYSVEQAKLPESEKRIIR  
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DKYSFORYTSMNCEATSHKSEKQOQSEKSGOYRISQOFVPEPTEKSGVNGVEA  
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BASE COUNT 3599 a 2281 c 2387 g 3226 t  
ORIGIN  
Query Match 52.0%; Score 53.6; DB 10; Length 11493;  
Best Local Similarity 73.9%; Pred. No. 6.9e-05;

	Matches	68:	Conservative	0:	Mismatches	24:	Indels	0:	Gaps	0:
OY	1	GAAGTACTGCAATACAGTTTAATGCACGATTAAAGCTCCTCGATATGTGAATGCT	60							
Db	6467	GAAGTGACTGGAAATAAAGATTTAATGACAGCATTAAATGACACCGCATATGTGAGTTAC	6526							
OY	61	AATACAGTTAAAAAACGGTTTTTCGCCGTT	92							
Db	6527	TAAATCACGTTAAAAAACGGTATTTCCTCGGT	6558							

  

	RESULT 7	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	JOURNAL	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
	AC138718/c	AC138718	283096 bp DNA linear HTG 25-FEB-2003												
			Mus musculus chromosome UKK clone RP23-221F8, WORKING DRAFT												
			SEQUENCE, 4 unordered pieces.												
			AC138718												
			AC138718.1 GI:27753855												
			HMG; HTGS_PHASEI; HTGS_DRAFT; HTGS_FUZZTOP.												
			Mus musculus (house mouse)												
			Mus musculus												
			Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;												
			Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.												
			1 (bases 1 to 283096)												
			McPherson,J.D. and Waterston,R.H.												
			The sequence of Mus musculus clone												
			Unpublished												
			2 (bases 1 to 283096)												
			McPherson,J.D. and Waterston,R.H.												
			Direct Submission												
			Submitted (15-JUN-2003) Genome Sequencing Center, 4444 Forest Park												
			Parkway, St. Louis, MO 63108, USA												
			3 (bases 1 to 283096)												
			Mcpherson,J.D. and Waterston,R.H.												
			Direct Submission												
			Submitted (25-FEB-2003) Genome Sequencing Center, 4444 Forest Park												
			Parkway, St. Louis, MO 63108, USA												
			Genome Center												
			Center: Washington University Genome Sequencing Center												
			Center code: WUGSC												
			Web site:http://genome.wustl.edu/gsc/index.shtml												
			Contact: submissions@wustl.wustl.edu												
			Project Information												
			Center project name: M.BAO221PF08												
			Summary Statistics												
			Sequencing vector: MI3; O%												
			Sequencing vector: Plasmid; 100%												
			Chemistry: Dye-primer ET; 0% of reads												
			Chemistry: Dye-terminator Big Dye; 100% of reads												
			Assembly program: Phrap; version 0.990319												
			Consensus quality: 282412 bases at least Q40												
			Consensus quality: 283029 bases at least Q20												
			Insert size: 218000; agarose-fp												
			Quality coverage: 18.55 in Q20 bases; sum-of-contigs												
			Quality coverage: 12.13 in Q20 bases; sum-of-contigs												
			NOTE: This is a working draft												

<b>FEATURES</b>	* 154353:	gap of unknown length.
	* 154354	283096: contig of 128743 bp in length.
<b>SOURCE</b>	Location/Qualifiers	
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	33805..85933	/note="assembly_name:Contig51"
	86034..134253	/note="assembly_name:Contig52"
	154354..283096	/note="assembly_name:Contig53"
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Query Match	52.0%;	Score 53.6; DB 2; Length 283096;
Best Local Similarity	73.9%;	Pred. No. 4.7e-05;
Matches	68; Conservative	0; Mismatches 24; Indels 0; Gaps 0;
OY	1 GAATGACGTGAATTACAGCTTTAATGACAGCACTTAATAGCTCCTGCATATGCAATTGCT 60	
Db	249129 GAATGACGTGAATTAAATAGTTTAAAGACAGCACTTAATAGCACCTGCATATGTTGAGTTAC 249070	
OY	61 AATACAGTTAAAAAACGGTATTTCCCTGGTT 92	
Db	249069 TAATCGAGTTAAAAAACGGTATTTCCCTGGT 249038	
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LOCUS	BV018667	722 bp DNA linear SRS 30-MAY-2003
DEFINITION	S212P624DPH4.T0 CZECHII/EI Mus musculus STS genomic, sequence tagged site.	
ACCESSION	BV018667	
VERSION	BV018667.1	GI:31102562
KEYWORDS	STS.	
SOURCE	Mus musculus (house mouse)	
ORGANISM	Mus musculus	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.	
AUTHORS	I. (bases 1 to 722)	
TITLE	Wade,C.M., Kulbokas,E.J. III, Kirby,A.W., Zody,M.C., Mullikin,J.C., Lander,E.S., Lindblad-Toh,K. and Daly,M.J.	
JOURNAL	The mosaic structure of variation in the laboratory mouse genome	
MEDLINE	Nature 420 (5915), 574-578 (2002)	
PUBMED	22354684	
COMMENT	12466852	
	Contact: Kerstin Lindblad-Toh Whitehead Institute for Biomedical Research, Center for Genome Research 320 Charles Street, Cambridge, MA 02141, USA Tel: 6172521477 Fax: 6172580903 Email: kersll@genome.wi.mit.edu Primer A: None Primer B: None STS size: 722 Protocol: WGS-discovery: Paired-end low-coverage whole genome shotgun reads were generated from 129S1/SvImJ, C3H/HeJ, and BALB/cByJ. The WGS reads were placed uniquely on the MGSCv3 C57BL/6J assembly and SNP detection was carried out by SSAHA-SNP. 225,000 reads were annotated as STSs and 81,000 SNPs were associated with alleles from C57BL/6J and the strain from which the particular read came. The validation rate for these SNPs was estimated at approximately 98%. Location/Qualifiers	

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ORIGIN

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Best Local Similarity 91.2% Pred. No. 0.0018;
Matches 52; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GAAGTACTGGAATACAGTTTAATGACAGCATTAATAGCTCGCATATGTAAT 57
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RESULT 9
AC126559 240277 bp DNA linear HTG 09-MAY-2003
LOCUS Rattus norvegicus clone CH230-4E7, *** SEQUENCING IN PROGRESS ***
DEFINITION 2 unordered pieces.
AC126559.5 GI:30466790
VERSION HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
KEYWORDS Rattus norvegicus (Norway rat)
SOURCE Rattus norvegicus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 240277)
Muzny,D,Marie, Metzger,M, Lee, Abramson,S, Adams,C, Alder,J,
Allen,C, Allen,H, Alsbrooks,S, Amin,A, Angiano,D,
Ayala-Bechli,Y, Aoyagi,A, Ayodeji,M, Baca,E, Baden,H,
Baldwin,D, Bandaranaike,D, Barber,M, Barnstead,M, Benahmed,F,
Biswal,K, Blair,J, Blankenburg,K, Blyth,P, Brown,M,
Bryant,N, Buhay,C, Burch,P, Burrell,K, Calderon,E,
Cardenas,Y, Carter,K, Cavazos,I, Ceasar,H, Center,A,
Chacko,J, Chavez,D, Chen,G, Chen,R, Chen,Y, Chen,Z, Chu,J,
Cleveland,C, Cockrell,R, Cox,C, Coyle,M, Cree,A, D'Souza,L,
Devila,M,L, Davis,C, Davy-Carroll,L, De Anda,C, Dederich,D,
Delgado,O, Denson,S, Deramo,C, Ding,Y, Dinh,H, Divya,K,
Draper,H, Dugan-Rocha,S, Dunn,A, Durbin,K, Duval,B, Eaves,K,
Egan,A, Escotto,M, Eugene,C, Evans,C,A, Falls,T, Fan,G,
Fernandez,S, Finley,M, Flagg,N, Forbes,L, Foster,M, Foster,P,
Fraser,C,M, Gabisi,A, Ganta,R, Garcia,A, Garner,T, Garza,M,
Geregeorgis,E, Geer,K, Gill,R, Grady,M, Guerra,W, Guevara,W,
Guarante,P, Haaland,W, Hamill,C, Hamilton,C, Hamilton,K,
Harvey,Y, Havlak,P, Hawes,A, Henderson,N, Hernandez,K,
Hernandez,R, Hines,S, Hladun,S,L, Hodgson,A, Hogues,M,
Hollins,B, Howells,S, Huliy,S, Hume,J, Idlebird,D, Jackson,A,
Jackson,L, Jacob,L, Jiang,H, Johnson,B, Johnson,R, Jolivet,A,
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Kowis,C, Kraft,C,L, Lebow,H, Levan,J, Lewis,L, Li,Z, Liu,J,
Liu,J, Liu,W, Liu,Y, London,P, Longacre,S, Lopez,J,
Lorensuhewa,L, Louiseged,H, Lozado,R,J, Lu,X, Ma,J,
Maheshwari,M, Mahindartne,M, Mahmoud,M, Malloy,K, Mangum,A,
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Mannley,S, McLeod,M,P, McNeill,T,Z, Meenen,E,
Milosavljevic,A, Miner,G, Minja,E, Montemayor,J, Moore,S,
Morgan,M, Morris,K, Morris,S, Munidasa,M, Murphy,M, Nair,L,
Nankervis,C, Neal,D, Newton,N, Nguyen,N, Norris,S,
Naokoelameh,O, Okuwon,G, Olarunpusoon,A, Pal,S, Parks,K,
Pasternak,S, Paul,H, Perez,A, Perez,L, Plannoch,C,
Plopper,F, Polidexter,A, Popovic,D, Primus,E, Pu,L,L,
Puzio,B, Quiroz,J, Rachlin,E, Reeves,K, Regier,M,A, Reigh,R,
Reilly,M, Reilly,M, Ren,Y, Reuter,M, Richards,S, Riggs,F,
Rives,C, Rodkey,T, Rojas,A, Rose,M, Rose,R, Ruiz,S,J,
Sanders,W, Savery,G, Scherer,S, Scott,G, Shatsman,S, Shen,H,
Shetty,J, Shwartsbeyn,A, Sisson,I, Sitter,C,D, Smajs,D,

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TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Sneed,A., Sodergren,E., Song,X.-Z., Sorelle,R., Sosa,J.,
Steinle,M., Strong,R., Sutton,A., Sytek,A., Taber,P., Taylor,C.,
Taylor,T., Thomas,N., Thomas,S., Tinney,A., Trejos,Z., Usmani,K.,
Vals,R., Vera,V., Villasana,D., Waldron,L., Walker,B., Wang,J.,
Wang,Q., Wang,S., Warren,J., Warren,R., Wei,X., White,F.,
Williams,G., Willson,R., Wleczyk,R., Wooden,H., Worley,K.,
Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,D., Yoon,V.,
Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von
Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O.,
Weinstock,G. and Gibbs,R.A.
Direct Submission
Unpublished
2 (bases 1 to 240277)
Worley,K.C.
Direct Submission
Submitted (07-JUN-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 240277)
Rat Genome Sequencing Consortium.
Submitted (09-MAY-2003) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On May 9, 2003 this sequence version replaced gi:25188888.
The sequence in this assembly is a combination of BAC based reads
and whole genome shotgun sequencing reads assembled using Atlas
(http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described
in the feature table below represents a scaffold in the Atlas
assembly (a 'contig-scaffold'). Within each contig-scaffold,
individual sequence contigs are ordered and oriented, and separated
by sized gaps filled with Ns to the estimated size. The sequence
may extend beyond the ends of the clone and there may be sequence
contigs within a contig-scaffold that consist entirely of whole
genome shotgun sequence reads. Both end sequences and whole genome
shotgun sequence only contigs will be indicated in the feature
table.
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GATV
Center clone name: CH230-4E7
----- Summary Statistics
Assembly program: Atlas
Consensus quality: 228324 bases at least Q40
Consensus quality: 230189 bases at least Q30
Consensus quality: 231614 bases at least Q20
Estimated insert size: 240669; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
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* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 2 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 239107: contig of 239107 bp in length
* 239108 239207: gap of unknown length
* 239208 240277: contig of 1070 bp in length.
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| | | | |  
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UTG 13-TTT-2000	

VERSION	DEFINITION	ACCESSION
AC021908.2	Homo sapiens, clone RP11-21621, LOW-PASS SEQUENCE SAMPLING.	GI:9123999
AC021908		

RELATIONS	into, into_into:
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens

REFERENCE

1 (bases 1 to 92309)

Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

TITLE	JOURNAL
Homo sapiens, clone RP11-21G21	Unpublished
2 (bases 1 to 82308)	

**AUTHORS**  
Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Boduslavsky, L., Boukhalter, B., Brown, A., Burkett, G., Castile, A.

Choepeh, I., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Dearellano, K., Dewar, K., Domino, M., Doyle, M., Fenebor, J., Ferreira, P., FitzHugh, W., Forrest, C., Gage, D., Galagan, J.,

Howland, J. C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Landers, T., Lehoczký, J., Levine, R., Lieu, C., Liu, G., Locke, K.,

McPheeters, R., Meldrim, J., Meneus, L., Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Olivari, T.M., Peterson, K., Pierce, N., Pisan, C., Pollock, V., Rumond, C., Rutter, B., Seaburn, D.

Roy, A., Santos, R., Severy, P., Spencer, B., Stojanovic, N., Subramanian, A., Talmas, J., Tirrell, A., Vassiliev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W., J. Tirrell, A., Vassiliev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W., J.

TITLE  
JOURNAL  
Submitted (22-JAN-2000) Whitehead Institute/MIT Center for Genome  
Zimmer, A. and Zou, M.  
Direct Submission

COMMENT  
On Jul 13, 2000 this sequence version replaced gi:5730876.  
All repeats were identified using RepeatMasker:

<http://ftp.genome.washington.edu/RM/RepeatMasker.html>  
----- Genome Center  
Cotton, Whitcomb Institute / Wm. Center for Genome Research

Center code: MIBR  
Web site: <http://www-seq.wi.mit.edu>  
Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)

```
----- Project information
Center project name: L4008
Center clone name: 21_G_21
```

\* NOTE: This record contains 91 individual  
\* sequencing reads that have not been assembled into

\* and the order in which they appear is completely

- \* arbitrary, low-pass sequence sampling is useful for
- \* identifying clones that may be generic and allow
- \* overlap relationships among clones to be deduced.
- \* However, it should not be assumed that this clone
- \* will be sequenced to completion. In the event that
- \* the record is updated, the accession number will
- \* be preserved.

	914: contig of 914 bp in length
1	1014: gap of 100 bp
915	1937: contig of 923 bp in length
1015	2037: contig of 100 bp in length
1025	2037: contig of 100 bp in length

*	1938	2037:	gap of 100 bp
*	2038	2974:	contig of 937 bp in length
*	2975	3074:	gap of 100 bp
*	3075	3993:	contig of 919 bp in length

	3075	3555	4093	4989
*	contig of 515 bp in length	contig of 100 bp	contig of 895 bp in length	gap of 100 bp
*				
*				
*				

	contig	length
5089	6006: contig of 918 bp	in length
6007	6106: gap of 100 bp	
6107	7012: contig of 906 bp	in length

*	7013	7112: gap of 100 bp
*	7113	8033: contig of 921 bp in length
*	8034	8133: gap of 100 bp

	contig of 918 bp in length	gap of 100 bp	contig of 935 bp in length	contig of 100 bp
8134	9051:			
9052		9151:		
9152		10086:		
10087		10186:		

11190 12084: contig of 895 bp in length  
 \* 11090 11189: gap of 100 bp  
 \* 10187 11089: contig of 903 bp in length  
 \* 10087 10186: gap of 100 bp  
 \*

	12085	12185	13118
12085	12085: gap of 100 bp	13117: contig of 933 bp in length	13217: gap of 100 bp
12185	12184: contig of 100 bp	13117: contig of 933 bp in length	13217: gap of 100 bp
13118	12085: gap of 100 bp	13117: contig of 933 bp in length	13217: gap of 100 bp

*	13218	14110: contig of 893 bp in length
*	14111	14210: gap of 100 bp
*	14211	15120: contig of 910 bp in length

*	15121	15220: gap of 100 bp
*	15221	16155: contig of 935 bp in length
*	16156	16255: gap of 100 bp
*	16356	17187: contig of 832 bp in length

*	18207	18306: gap of 100 bp
*	17288	18206: contig of 919 bp in length
*	17188	17287: gap of 100 bp
*	16236	17187: contig of 932 bp in length

	18307	19241	19341
*	19240: contig of 934 bp	19340: gap of 100 bp	20262: contig of 922 bp
*	5-17		
*	19240: contig of 934 bp	19340: gap of 100 bp	20262: contig of 922 bp

	20362: gap of 100 bp	20362: gap of 100 bp
20263	20362: gap of 100 bp	20362: gap of 100 bp
20363	21267: contig of 905 bp	21267: contig of 905 bp
21268	21367: gap of 100 bp	21367: gap of 100 bp

	contlg of 904 bp	in length
21368	22271:	contlg of 904 bp
22272	22371:	gap of 100 bp
22372	23280:	contlg of 909 bp
23281	23280:	gap of 100 bp

*	24401	25318: contig of 918 bp in length
*	24301	24400: gap of 100 bp
*	23381	24300: contig of 920 bp in length
*	23281	23380: gap of 100 bp
*	23281	

	25319	25419	26341
*	25318: contig of 100 bp	26340: contig of 922 bp	26440: gap of 100 bp
*			
*			
*			

	contig of 893 bp in length
* 26441	27333: contig of 893 bp in length
* 27334	27433: gap of 100 bp
* 27434	28339: contig of 906 bp in length

	28340	28439: gap of 100 bp
*	28340	28439: gap of 100 bp
*	28440	29335: contig of 896 bp in Length
*	29336	29335: gap of 100 bp
*	29337	29336: gap of 100 bp

	30361: contig of 926 bp in length	30461: gap of 100 bp	31348: contig of 887 bp in length	31448: ran of 100 bp
*	29436			
*	30362			
*	30462			
*	31349			

	gap of 100 bp	contig of 938 bp	contig of 925 bp
31345	31440	32386	33411
31449		32486	
32387			
32487			

\* 33412 33511: gap of 100 bp

```

* 33512 34425: contig of 914 bp in length
* 34426 34525: gap of 100 bp
* 34526 35410: contig of 885 bp in length
* 35410 35510: gap of 100 bp
* 35510 36426: contig of 916 bp in length
* 36426 36527: gap of 100 bp
* 36527 37434: contig of 907 bp in length
* 37434 37533: gap of 100 bp
* 37533 38477: contig of 944 bp in length
* 38477 38577: gap of 100 bp
* 38577 39478: contig of 901 bp in length
* 39478 39579: gap of 100 bp
* 39579 40485: contig of 907 bp in length
* 40485 40585: gap of 100 bp
* 40585 41532: contig of 947 bp in length
* 41532 41632: gap of 100 bp
* 41632 42546: contig of 914 bp in length
* 42546 42647: gap of 100 bp
* 42647 43567: contig of 921 bp in length
* 43567 43667: gap of 100 bp
* 43667 44591: contig of 924 bp in length
* 44591 44691: gap of 100 bp
* 44691 45591: contig of 900 bp in length
* 45591 45692: gap of 100 bp
* 45692 46615: contig of 924 bp in length
* 46615 46715: gap of 100 bp
* 46715 47612: contig of 897 bp in length
* 47612 47713: gap of 100 bp
* 47713 48632: contig of 920 bp in length
* 48632 48732: gap of 100 bp
* 48732 49654: contig of 922 bp in length
* 49654 49754: gap of 100 bp
* 49754 50648: contig of 894 bp in length
* 50648 50749: gap of 100 bp
* 50749 51644: contig of 896 bp in length
* 51644 51744: gap of 100 bp
* 51744 52675: contig of 931 bp in length
* 52675 52775: gap of 100 bp
* 52775 53719: contig of 944 bp in length
* 53719 53819: gap of 100 bp
* 53819 54715: contig of 896 bp in length
* 54715 54815: gap of 100 bp
* 54815 55729: contig of 914 bp in length
* 55729 55829: gap of 100 bp
* 55829 56761: contig of 932 bp in length
* 56761 56861: gap of 100 bp
* 56861 57754: contig of 893 bp in length
* 57754 57854: gap of 100 bp
* 57854 58754: contig of 900 bp in length
* 58754 58854: gap of 100 bp
* 58854 59778: contig of 924 bp in length
* 59778 59878: gap of 100 bp
* 59878 60804: contig of 926 bp in length
* 60804 60904: gap of 100 bp
* 60904 61841: contig of 937 bp in length
* 61841 61941: gap of 100 bp
* 61941 62870: contig of 929 bp in length
* 62870 62970: gap of 100 bp
* 62970 63885: contig of 915 bp in length
* 63885 63985: gap of 100 bp
* 63985 64902: contig of 917 bp in length
* 64902 65002: gap of 100 bp
* 65002 65914: contig of 912 bp in length
* 65914 66014: gap of 100 bp
* 66014 66918: contig of 904 bp in length
* 66918 67018: gap of 100 bp
* 67018 67931: contig of 913 bp in length
* 67931 68031: gap of 100 bp
* 68031 68901: contig of 870 bp in length
* 68901 69001: gap of 100 bp
* 69001 69902: contig of 901 bp in length
* 69902 70002: gap of 100 bp
* 70002 70936: contig of 934 bp in length

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```

* 70937 71036: gap of 100 bp
* 71037 71937 71936: contig of 900 bp in length
* 71937 72036: gap of 100 bp
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Best Local Similarity 65.58; Score 37.6; DB 2; Length 92309;
Matches 55; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

Qy 18 AGTTTATGACGACATTATAGCTCGCATATGTGATGATGCTAATACAGTTAAACAAAC 77
Db 91089 AGTGTATATAGTACATGCAATGCTGTCTGTCTTAAGTGTATGATGCAAAATACATTAAAGAAAC 91148

Qy 78 GGATTTTCCCTGGTCTGATCAAA 101
Db 91149 AGTATTCCTGCTGGCATATCAAA 91172

RESULT 11
AR253940/c AR253940 74962 bp DNA linear PAT 20-DEC-2002
LOCUS Sequence 3 from patent US 6479270.
ACCESSION AR253940
VERSION AR253940.1 GI:27302425
KEYWORDS
SOURCE
ORGANISM
Unclassified.
REFERENCE
1 (bases 1 to 74962)
AUTHORS
Wei,M.-H., Ketchum,K.A., Di Francesco,V. and Beasley,E.M.
TITLE
Isolated human phosphatase proteins, nucleic acid molecules
encoding human phosphatase proteins, and uses thereof
JOURNAL Patent: US 6479270-A 3 12-NOV-2002;
FEATURES
source 1. 74962
BASE COUNT 21639 a 14055 c 14307 g 24824 t 137 others
ORIGIN

Query Match
Best Local Similarity 62.98; Pred. No. 3 6; Length 74962;
Matches 56; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

Qy 12 AATACAGTTTATGACGACATTATAGCTCGCATATGTGATGATGCTAATACAGTTAA 71
Db 63338 AAAAAAATAATTCACACATCAAGACCTAGAGACTTACTTTCAATCAATTA 63279

Qy 72 AAAACGTAATTCCTGGTCTGATCA 100
Db 63278 AAAAAGCTTTCAGTACTTCATCTCA 63250

RESULT 12
AX350371/c AX350371 74962 bp DNA linear PAT 06-FEB-2002
LOCUS Sequence 3 from Patent WO0160992.
DEFINITION AX350371
ACCESSION AX350371
VERSION AX350371.1 GI:18616029
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS
Wei,M.-H., Ketchum,K.A., di Francesco,V.C. and Beasley,E.M.
TITLE
Human protein tyrosine phosphatase; encoding dna and uses thereof
JOURNAL Patent: WO 0160992-A 3 23-AUG-2001;
PE Corporation (NY) (US)
FEATURES
location/Qualifiers
1. 74962
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 21639 a 14055 c 14307 g 24824 t 137 others

```



Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., De Souza, L., Davila, M. L., Davis, S., Day-Carroll, L., De Anda, C., Dedrich, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dihn, H., Divya, K., Draper, H., Dugan-Rocha, S., Dunn, A., Durkin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Eugene, C., Evans, C. A., Falls, T., Fan, G., Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P., Fraser, C. M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Georgogiorgis, E., Geer, K., Gill, R., Grady, M., Guerra, N., Guerafara, M., Guerin, P., Haaland, M., Hamill, C., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Hernandez, R., Hines, S., Hladun, S. L., Hodgson, A., Hogues, M., Hollins, B., Howells, S., Huliy, S., Hume, J., Idlebird, D., Jackson, L., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A., Karpachy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kwis, C., Kraft, C. L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, Y., Liu, Y., London, P., Longacre, S., Lopez, J., Lorenshuewa, L., Louisedge, H., Lozada, R. J., Lu, X., Ma, J., Maheshwari, M., Mahindartine, M., Mahmood, M., Malloy, K., Mangum, A., Mangum, B., Mapue, P., Martin, K., Martin, R., Martinez, E., Manthey, S., McLeod, M. P., McNeill, T. Z., Meenen, E., Mogensavljevic, A., Miner, G., Minji, E., Montemayor, J., Moore, S., Morris, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nair, L., Nakevici, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Nwackemeh, O., Okwuonu, G., Olarunpungson, A., Pal, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Piankocch, C., Plopper, F., Poindeexter, A., Popovic, D., Prinus, E., Pu, L., L., Puzo, M., Quito, J., Rachlin, E., Reeves, K., Reigel, M. A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S., Sanders, W., Savary, G., Scherer, S., Scott, G., Shatman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C. D., Smaj, S. D., Sneed, A., Sodergren, E., Song, X. Z., Sorelle, R., Sosa, J., Steimle, M., Strong, R., Sutton, A., Svatek, A., Tabot, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tinney, A., Trejos, Z., Usmani, K., Valas, R., Vera, Y., Villasa, D., Waldron, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wleczyk, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederhauser, A., Weiss, R., Smith, D. R., Holt, R. A., Smith, H. O., Weinstein, G. A. and Gibbs, R. A.

Direct Submission

Unpublished

2 (bases 1 to 291738)

Worley, K. C.

Direct Submission

Submitted (23-OCT-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 291738)

Rat Genome Sequencing Consortium.

Direct Submission

Submitted (10-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On May 10, 2003 this sequence version replaced g1:24818859. The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center

Center: Baylor College of Medicine

Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>

Contact: [hgsc.help@bcm.tmc.edu](mailto:hgsc.help@bcm.tmc.edu)



JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 156547)  
 AUTHORS McPherson, J.D. and Waterston, R.H.  
 TITLE Direct Submission  
 JOURNAL Submitted (08-APR-2002) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA  
 REFERENCE 3 (bases 1 to 156547)  
 AUTHORS McPherson, J.D. and Waterston, R.H.  
 TITLE Direct Submission  
 JOURNAL Submitted (21-MAY-2002) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA  
 REFERENCE 4 (bases 1 to 156547)  
 AUTHORS McPherson, J.D. and Waterston, R.H.  
 TITLE Direct Submission  
 JOURNAL Submitted (21-JUN-2002) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA  
 COMMENT On May 16, 2002 this sequence version replaced gi:20069850.

FEATURES  
 source 1. 156547  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:10090"  
 /clone="RP24-537M7"  
 BASE COUNT 47059 a 32654 c 31502 g 45332 t  
 ORIGIN

Query Match 32.8%; Score 33.8; DB 10; Length 156547;  
 Best Local Similarity 58.4%; Pred. No. 15;  
 Matches 59; Conservative 0; Mismatches 42; Indels 0; Gaps 0;  
 QY 1 GAAGTGCATGCAATTAACAGTTTAATGACAGCATTAATGCTCCGTCATATGTAATGCT 60  
 DB 139738 GTATTGGCTTTAGCAACATATTCATTATTCATTGTTAACTATTGATCAAGTAATTTGGG 139797  
 QY 61 AATACAGTTAAATAAAGCGTATTTCCCGTTCGATCCAA 101  
 DB 139798 AGTATTTCTATAAATGATTTTATTTAGAGGTTCTGAGTCAA 139838

RESULT 16  
 AL928639/c 177843 bp DNA linear ROD 31-OCT-2002  
 LOCUS Mouse DNA sequence from clone RP23-446017 on chromosome 2, complete  
 DEFINITION sequence.  
 ACCESSION AL928639  
 VERSION AL928639.5 GI:24474486  
 KEYWORDS HTG.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 177843)  
 Bates, K.  
 Direct Submission  
 Submitted (31-OCT-2002) Wellcome Trust Sanger Institute, Hinxton,  
 Cambridgeshire, CB10 1SA, UK. E-mail enquiries:  
 humquerry@sanger.ac.uk  
 On Nov 1, 2002 this sequence version replaced gi:24414771.  
 COMMENT ----- Genome Center  
 Center: Wellcome Trust Sanger Institute  
 Center code: SC  
 Web site: <http://www.sanger.ac.uk>  
 Contact: humquerry@sanger.ac.uk

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.  
 This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: EMBL, Sw: SWISSPROT, Tr: TREMBL, Wp: WORMPEP. Information on the WORMPEP database can be found at  
[http://www.sanger.ac.uk/Projects/C\\_elegans/wormpep](http://www.sanger.ac.uk/Projects/C_elegans/wormpep) RP23-446017 is from the RPCI-23 Mouse PAC library  
 constructed by the group of Pieter de Jong.  
 For further details see <http://www.chori.org/bacpac/home.htm>  
 VECTOR: pBACe3.6.

FEATURES  
 source 1. 177843  
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 /mol\_type="genomic DNA"  
 /db\_xref="taxon:10090"  
 /chromosome="2"  
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 /clone\_11b="RPCI-23"  
 BASE COUNT 52840 a 36061 c 35495 g 53447 t  
 ORIGIN

Query Match 32.8%; Score 33.8; DB 10; Length 177843;  
 Best Local Similarity 58.4%; Pred. No. 15;  
 Matches 59; Conservative 0; Mismatches 42; Indels 0; Gaps 0;  
 QY 1 GAAGTGCATGCAATTAACAGTTTAATGACAGCATTAATGCTCCGTCATATGTAATGCT 60  
 DB 127561 GTATTGGCTTTAGCAACATATTCATTATTCATTGTTAACTATTGATCAAGTAATTTGGG 127502  
 QY 61 AATACAGTTAAATAAAGCGTATTTCCCGTTCGATCCAA 101  
 DB 127501 AGTATTTCTATAAATGATTTTATTTAGAGGTTCTGAGTCAA 127461

RESULT 17  
 BX284649/c 248044 bp DNA linear HTG 08-MAY-2003  
 LOCUS Mus musculus chromosome 2 clone RP23-42M7, \*\*\* SEQUENCING IN  
 DEFINITION PROGRESS \*\*\*, 3 unordered pieces.  
 ACCESSION BX284649  
 VERSION BX284649.11 GI:30519649  
 KEYWORDS HTG; HTGS; PHASE1; HTGS; ACTIVERFIN; HTGS\_DRAFT; HTGS\_FULLTOP.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 248044)  
 Johnson, C.  
 Direct Submission  
 Submitted (07-MAY-2003) Wellcome Trust Sanger Institute, Hinxton,  
 Cambridgeshire, CB10 1SA, UK. E-mail enquiries:  
 humquerry@sanger.ac.uk  
 On May 10, 2003 this sequence version replaced gi:30550058.  
 Sequence from the Mouse Genome Sequencing Consortium whole genome  
 shotgun may have been used to confirm this sequence. Sequence data  
 from the whole genome shotgun alone has only been used where it has  
 a phred quality of at least 30.  
 COMMENT ----- Genome Center  
 Center: Wellcome Trust Sanger Institute  
 Center code: SC  
 Web site: <http://www.sanger.ac.uk>

Contact: humquerry@esanger.ac.uk  
 ----- Project Information  
 Center project name: BM42M7  
 ----- Summary Statistics  
 Assembly program: XGAP4; version 4.5  
 Chemistry: Dye-terminator; 100% of reads  
 Consensus quality: 247687 bases at least Q40  
 Consensus quality: 247768 bases at least Q30  
 Consensus quality: 247797 bases at least Q20  
 Insert size: 247844; sum-of-coverage  
 Insert size: 223039; 6.2% error; agarose-fp  
 Quality coverage: 10.25% in Q20 bases; sum-of-coverage  
 Quality coverage: 11.3% in Q20 bases; agarose-fp  
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 \* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 3 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.  
 \*  
 \* 1 168564: contig of 168564 bp in length  
 \* 168565 168664: gap of 100 bp  
 \* 168665 191685: contig of 23021 bp in length  
 \* 191686 191785: gap of 100 bp  
 \* 191786 248044: contig of 56259 bp in length.  
 \* Location/Qualifiers  
 1. 248044  
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 /mol\_type="genomic DNA"  
 /db\_xref="taxon:10090"  
 /chromosome="2"  
 /clone\_lib="RP23-42M7"  
 /clone\_id="RP23-23"  
 1. 168564  
 /note="assembly fragment:03578  
 fragment\_chain:1"  
 misc-feature  
 168665..191685  
 /note="assembly fragment:03428  
 fragment\_chain:1"  
 191786..248044  
 /note="assembly fragment:03589"  
 BASE COUNT 72534 a 48203 c 50482 g 76625 t 200 others  
 ORIGIN  
 Query Match 32.8%; Score 33.8; DB 2; Length 248044;  
 Best Local Similarity 58.4%; Pred. No. 15;  
 Matches 59; Conservative 0; Mismatches 42; Indels 0; Gaps 0;  
 Oy 1 GAAGTACGTGAATAACAGTATTATGACAGCATTAACTGCTGATATGGAATTGCT 60  
 1  
 Db 26808 GATATGCCCTTGTGACACATATTTATTCATTTGTTACTATGATCAAGTAATTGGG 26749  
 1  
 Oy 61 AATACAGTAAAAAAGGATTTCCCTGGTCTGATCCA 101  
 1  
 Db 26748 AGTATTTTCTATTAATAATGATTTTATGAGGTTCTGATCA 26708  
 1  
 RESULT 18  
 AC134425/c 172022 bp DNA 1linear HTG 12-MAR-2003  
 LOCUS  
 DEFINITION Mus musculus clone RP24-266E5, WORKING DRAFT SEQUENCE, 5 unordered  
 pieces.  
 AC134425 GI:28927764  
 VERSION AC134425.3  
 KEYWORDS HTG: HTGS PHASE1: HTGS DRAFT.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 172022)  
 Birren,B., Nusbaum,C. and Lander,E.

# TITLE JOURNAL REFERENCE AUTHORS

Mus musculus, clone RP24-266E5  
 Unpublished  
 2 (bases 1 to 172022)  
 Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S.,  
 Barne,N., Bastien,V., Bloom,T., Boguslavsky,L., Boukhalter,B.,  
 Camarata,J., Chang,J., Chazaro,B., Choepel,Y., Collymore,A.,  
 Cook,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S.,  
 Faro,S., Ferreira,P., Fitzgerald,M., Gage,D., Galagan,J.,  
 Gardyna,S., Gord,S., Graham,L., Grand-Pierre,N., Hacos,B.,  
 Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A.,  
 Karatas,A., Kells,C., Landers,T., Levine,R., Lindblad-Toh,K.,  
 Liu,G., Maclean,C., Macdonald,P., Major,J., Matthews,C.,  
 McCarthy,M., Meldrum,J., Menus,L., Mihova,T., Mienga,V., Murphy,T., Naylor,J.,  
 O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J., Peterson,K.,  
 Plunkhang,P., Pierre,N., Raymond,C., Retta,R., Rise,C., Rogov,P.,  
 Roman,J., Roy,A., Schauer,S., Schuppach,R., Seaman,S., Severy,P.,  
 Smith,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Talamas,J.,  
 Testaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H.,  
 Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J.,  
 Zembek,L., Zimmer,A. and Zody,M.  
 Direct Submission

# TITLE JOURNAL REFERENCE AUTHORS

Submitted (26-SEP-2002) Whitehead Institute/MIT Center for Genome  
 Research, 320 Charles Street, Cambridge, MA 02141, USA  
 3 (bases 1 to 172022)  
 Birren,B., Nusbaum,C., Lander,E., Abouelleil,A., Allen,N.,  
 Anderson,S., Arachchi,H.M., Barne,N., Bastien,V., Bloom,T.,  
 Boguslavsky,L., Boukhalter,B., Camarata,J., Chang,J., Choepel,Y.,  
 Collymore,A., Cook,A., Cooke,P., Corum,B., Dearellano,K.,  
 Diaz,J.S., Dodge,S., Doolley,K., Dorris,L., Erickson,J., Faro,S.,  
 Ferreira,P., Fitzgerald,M., Gage,D., Galagan,J., Gardyna,S.,  
 Graham,L., Grand-Pierre,N., Hates,N., Hagopian,D., Hagos,B.,  
 Hall,J., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,  
 Kamat,A., Karatas,A., Kells,C., Landers,T., Levine,R.,  
 Lindblad-Toh,K., Liu,G., Lui,A., Mabbitt,R., Maclean,C.,  
 Macdonald,P., Major,J., Manning,J., Matthews,C., McCarthy,M.,  
 Meldrum,J., Menus,L., Mihova,T., Mienga,V., Murphy,T., Naylor,J.,  
 Nguyen,C., Nicol,R., Nordu,C., O'Connor,T., O'Donnell,P.,  
 O'Neill,D., Oliver,J., Peterson,K., Plunkhang,P., Pierre,N.,  
 Rachupka,A., Ramasamy,U., Raymond,C., Retta,R., Rise,C., Rogov,P.,  
 Roman,J., Schauer,S., Schuppach,R., Seaman,S., Severy,P., Smith,C.,  
 Spencer,B., Stange-Thomann,N., Stojanovic,N., Stubbs,M.,  
 Talamas,J., Testaye,S., Theodore,J., Topham,K., Travers,M.,  
 Vassiliev,H., Venkataraman,V.S., Viel,R., Vo,A., Wilson,B., Wu,X.,  
 Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.  
 Direct Submission

# TITLE JOURNAL COMMENT

Submitted (12-MAR-2003) Whitehead Institute/MIT Center for Genome  
 Research, 320 Charles Street, Cambridge, MA 02141, USA  
 On Mar 12, 2003 this sequence version replaced g1:28275012.  
 All repeats were identified using RepeatMasker:  
 Smit,A.F.A. & Green,P. (1996-1997)  
 http://ftp.genome.washington.edu/RM/RepeatMasker.html  
 ----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research  
 Center code: WIBR  
 Web site: http://www.seq.wi.mit.edu  
 Contact: sequence\_submissions@genome.wi.mit.edu

----- Project Information  
 Center project name: L27143  
 Center Clone name: 266\_E5

----- Summary Statistics  
 Sequencing vector: Plasmid; n/a; 100% of reads  
 Chemistry: Dye-terminator; Big Dye; 100% of reads  
 Assembly program: Phrap; version 0.960731  
 Consensus quality: 170825 bases at least Q40  
 Consensus quality: 171283 bases at least Q30  
 Consensus quality: 171504 bases at least Q20

Insert size: 174000; agarose-fp  
 Insert size: 171622; sum-of-coverage  
 Quality coverage: 9.2 in Q20 bases; agarose-fp  
 Quality coverage: 9.4 in Q20 bases; sum-of-coverage

\* NOTE: This is a 'working draft' sequence. It currently





320 Charles Street, Cambridge, MA 02141, USA

Tel: 6172521477

Fax: 6172560903

Email: kersl@genome.wi.mit.edu

Primer A: None

Primer B: None

STS size: 554

Protocol:

WGS-discovery: Paired-end low-coverage whole genome shotgun reads were generated from 12951/Symlu, C3H/HeJ, and BALB/cByJ. The WGS reads were placed uniquely on the MGSCV3 C57BL/6J assembly and SNP detection was carried out by SSMA-SNP. 225,000 reads were annotated as STSs and 81,000 SNPs were annotated with alleles from C57BL/6J and the strain from which the particular read came. The validation rate for these SNPs was estimated at approximately 98%.

#### FEATURES

source

Location/Qualifiers

1..554

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C3H/HeJ"

/db\_xref="taxon:10090"

/map="19 22-495 22440264-22440739"

/clone.lib="C3H/HeJ"

<1..>554

BASE COUNT 183 a 78 c 106 g 187 t

ORIGIN

Query Match

Best Local Similarity 31.8%; Score 32.8; DB 11; Length 554;

Matches 58; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 2 AAGTACGTCGATTAACAGCTTAATGACACCATTAATAGCTCCTGATGATGATGCTA 61

DB 269 AAAAAATTAATAATATTTTAAAGACGCTATCATAGCTCATGCTTATGATTAATTA 210

QY 62 ATACAGTTAAAAAAGCGTATTTCCCTGCTTCGATCCAA 101

DB 209 AAAAAATTAAAGAACTTAACCTCATTTATGTGACTCCA 170

RESULT 22

HS1110P6/c

LOCUS

DEFINITION Human DNA sequence from clone RP5-1110P6 on chromosome Xq21.1-22.3,

complete sequence.

ACCESSION AL049175

VERSION AL049175.12 GI:21212890

KEYWORDS HTG.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 40033)

AUTHORS Howden, P.

TITLE Direct Submission

JOURNAL Submitted (21-MAY-2002) Wellcome Trust Sanger Institute, Hinxton,

Cambridgeshire, CB10 1SA, UK. E-mail enquiries:

humquery@sanger.ac.uk Clone requests: clonerequests@sanger.ac.uk

On May 25, 2002 this sequence version replaced gi:5101738.

During sequence assembly data is compared from overlapping clones.

Where differences are found these are annotated as variations

together with a note of the overlapping clone name. Note that the

variation annotation may not be found in the sequence submission

corresponding to the overlapping clone, as we submit sequences with

only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all

regions were either double-stranded or sequenced with an alternate

chemistry or covered by high quality data (i.e., phred quality >=

30); an attempt was made to resolve all sequencing problems, such

as compressions and repeats; all regions were covered by at least

one plasmid subclone or more than one M13 subclone; and the

assembly was confirmed by restriction digest. The following

abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: EMBL; Sw: SWISSPROT; Tr: TrEMBL; Wp: WormPeP; Inf: Information on the WormPeP database can be found at

http://www.sanger.ac.uk/Projects/C\_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome X, constructed by the Sanger Centre Chromosome X Mapping

group. Further information can be found at

http://www.sanger.ac.uk/HGP/ChrX

RP5-1110P6 is from the library RPCT-5 constructed by the group of

Pleier de Jong. For further details see

http://www.chori.org/bacpac/home.htm

VECTOR: pCYPAC2.

FEATURES

source

Location/Qualifiers

1..40033

/organism="Homo sapiens"

/mol\_type="genomic DNA"

/db\_xref="RZPD:RPCTP704P061110"

/db\_xref="taxon:9606"

/chromosome="X"

/map="q21.1-22.3"

/clone="RP5-1110P6"

/clone.lib="RPCT-5"

BASE COUNT 14481 a 7019 c 7035 g 11498 t

ORIGIN

Query Match

Best Local Similarity 31.8%; Score 32.8; DB 9; Length 40033;

Matches 52; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 13 ATACAGTTTAATGACAGCTTAATAGCTCCTGATGATGATGCTTAATACAGTTAA 72

DB 39216 AATTCAGTTAAATGACAGCTTAATAGCTCCTGATGATGATGCTTAATACAGTTAA 72

QY 73 AAAAAAGTATTAATGACAGCTTAATAGCTCCTGATGATGATGCTTAATACAGTTAA 72

DB 39156 CAACCTGCACTTTCCAGATTTCTAA 39133

RESULT 23

AC141553

LOCUS

DEFINITION Rattus norvegicus clone CH230-123N13, \*\*\* SEQUENCING IN PROGRESS

AC141553

VERSION AC141553.1 GI:28975844

KEYWORDS HTG; HTGS\_PHASE1.

SOURCE Rattus norvegicus (Norway rat)

ORGANISM Rattus norvegicus; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

Rattus.

REFERENCE 1 (bases 1 to 156493)

AUTHORS

Allen, C., Allen, H., Aisbrooks, S., Amin, A., Anguiano, D.,

Anyalebech, V., Ayoyagi, A., Ayodeji, M., Baca, E., Baden, R.,

Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F.,

Biswal, K., Blair, J., Blankenburg, R., Blyth, P., Brown, M.,

Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E.,

Cardenas, V., Carter, K., Cavazos, I., Cesar, H., Center, A.,

Chacko, J., Chavez, D., Chen, C., Chen, R., Chen, Y., Chen, Z., Chu, J.,

Cleveland, C., Cockrell, R., Cox, C., Coyne, M., Gre, A., D Souza, L.,

Davila, M. L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D.,

Delgado, O., Denison, S., Deramo, C., Ding, Y., Dinh, H., Divya, K.,

Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K.,

Egan, A., Escotto, M., Eugene, C., Evans, C. A., Falls, T., Fan, G.,

Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P.,

Fraser, C. M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M.,

Gebregiorgis, E., Geer, K., Gill, R., Grady, M., Guerra, M., Guevara, W.,

Gunaratne, P., Haaland, W., Hamill, C., Hamilton, C., Hamilton, K.,

Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J.,

Hernandez, R., Hines, S., Hladun, S. L., Hodgson, A., Hogues, M.,

Hollins, B., Howells, S., Hulik, S., Hume, J., Ito, D., Jackson, A.,

Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A., Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovari, C., Kowis, C., Kraft, C., Ledow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Lorenshew, L., Louised, H., Lozano, R. J., Lu, X., Ma, J., Maheshwari, M., Mahindarane, M., Mahmoud, M., Malloy, K., Mangum, A., Mawney, S., McLeod, M., McNeill, T., Meenen, E., Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Mundasa, M., Murphy, M., Nair, L., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Nwokele, O., Okunolu, G., Olajunsgoon, A., Pal, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkuch, C., Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L., Puazo, M., Quito, J., Rachlin, E., Reeves, K., Regier, M., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rivers, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S. J., Sanders, M., Savary, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Slater, C. D., Smajs, D., Sneed, A., Sodergren, E., Song, X., Z., Sorrelle, R., Sosa, J., Steimle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Thigley, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villaseana, D., Waldron, L., Walker, B., Wang, J., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wlaczek, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, D., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D. R., Holt, R. A., Smith, H. O., Weinstock, G. and Gibbs, R. A.

Unpublished  
2 (bases 1 to 156493)  
Worley, K. C.

Direct Submission  
Submitted (17-Mar-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

----- Genome Center -----  
Center: Baylor College of Medicine  
Center code: BCM  
Web site: <http://www.hgsc.bcm.tmc.edu/>  
Contact: hgsc-help@bcm.tmc.edu  
----- Project Information -----  
Center project name: KRBX  
Center clone name: CH230-123N13  
----- Summary Statistics -----  
Sequencing vector: Plasmid  
Chemistry: Dye-terminator Big Dye 100% of reads  
Assembly program: Phrap; version 0.990329  
Consensus quality: 130692 bases at least Q40  
Consensus quality: 139963 bases at least Q40  
Consensus quality: 147828 bases at least Q20  
Estimated insert size: 135973; sum-of-coverage estimation  
Quality coverage: 2x in Q20 bases; sum-of-coverage estimation

\* NOTE: Estimated insert size may differ from sequence length  
(see [http://www.hgsc.bcm.tmc.edu/docs/genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html)).  
\* NOTE: This is a "working draft" sequence. It currently  
\* consists of 71 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

1 1857: contig of 1857 bp in length  
\* 1858 1957: gap of unknown length  
\* 1958 3564: contig of 1607 bp in length  
\* 3565 3664: gap of unknown length  
\* 3665 5132: contig of 1468 bp in length  
\* 5133 5232: gap of unknown length  
\* 5233 6236: contig of 1004 bp in length  
\* 6237 6336: gap of unknown length  
\* 6337 7825: contig of 1489 bp in length

7826 7925: gap of unknown length  
\* 7926 9500: contig of 1575 bp in length  
\* 9501 9600: gap of unknown length  
\* 9601 10817: contig of 1217 bp in length  
\* 10818 10917: gap of unknown length  
\* 10918 12217: contig of 1300 bp in length  
\* 12218 12318: gap of unknown length  
\* 12318 13580: contig of 1263 bp in length  
\* 13581 13680: gap of unknown length  
\* 13681 15147: contig of 1467 bp in length  
\* 15148 15247: gap of unknown length  
\* 15248 15607: contig of 1360 bp in length  
\* 15608 16707: gap of unknown length  
\* 16708 18076: contig of 1369 bp in length  
\* 18077 18176: gap of unknown length  
\* 18177 19193: contig of 1017 bp in length  
\* 19194 19293: gap of unknown length  
\* 19294 20517: contig of 1224 bp in length  
\* 20518 20617: gap of unknown length  
\* 20618 22094: contig of 1477 bp in length  
\* 22095 22194: gap of unknown length  
\* 22195 23313: contig of 1119 bp in length  
\* 23314 24834: gap of unknown length  
\* 24834 24934: gap of unknown length  
\* 24935 26737: contig of 1803 bp in length  
\* 26738 27952: contig of 1115 bp in length  
\* 27953 28052: gap of unknown length  
\* 28053 29433: contig of 1381 bp in length  
\* 29434 29534: gap of unknown length  
\* 29534 30847: contig of 1314 bp in length  
\* 30848 32471: contig of 1524 bp in length  
\* 32472 32571: gap of unknown length  
\* 32572 34474: contig of 1903 bp in length  
\* 34475 34575: gap of unknown length  
\* 34575 36825: contig of 2251 bp in length  
\* 36826 36925: gap of unknown length  
\* 36926 38141: contig of 1216 bp in length  
\* 38142 38241: gap of unknown length  
\* 38242 39344: contig of 1103 bp in length  
\* 39345 39444: gap of unknown length  
\* 39445 41224: contig of 1780 bp in length  
\* 41225 41324: gap of unknown length  
\* 41325 42495: contig of 1171 bp in length  
\* 42496 42595: gap of unknown length  
\* 42596 43688: contig of 1093 bp in length  
\* 43689 43788: gap of unknown length  
\* 43789 46090: contig of 2302 bp in length  
\* 46091 46190: gap of unknown length  
\* 46191 48101: contig of 1911 bp in length  
\* 48102 48201: gap of unknown length  
\* 48202 50073: contig of 1872 bp in length  
\* 50074 50173: gap of unknown length  
\* 50174 51801: contig of 1628 bp in length  
\* 51802 51902: gap of unknown length  
\* 51902 53447: contig of 1546 bp in length  
\* 53448 53547: gap of unknown length  
\* 53548 54893: contig of 1346 bp in length  
\* 54894 54993: gap of unknown length  
\* 54994 56795: contig of 1702 bp in length  
\* 56796 56995: gap of unknown length  
\* 56996 58715: contig of 1820 bp in length  
\* 58716 58716: gap of unknown length  
\* 58717 60729: contig of 2014 bp in length  
\* 60730 60829: gap of unknown length  
\* 60830 63324: contig of 2495 bp in length  
\* 63325 63424: gap of unknown length  
\* 63425 64814: contig of 1390 bp in length  
\* 64815 64914: gap of unknown length  
\* 64915 66140: contig of 1226 bp in length  
\* 66141 66240: gap of unknown length

TITLE  
JOURNAL  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Query Match	Best Local Similarity	Score	DB 2;	Length
Matches 47; Conservative	66.2%	Pred. No. 33;	Mismatches 24;	Indels 0; Gaps 0;
OY 14 TAACAGTTAATGACAGCATTAATAGCTCTCCATATGTGAATTGCTAATACAGTTAAAA				
Db 102012 TAACAGTTAATTTGATGATTAACACCTCTTTATTTCTGAATGCTCTATAGTTCCTA				
OY 74 AAACGTAATT 84				
Db 102072 AAACGTAATT 102082				

JOURNAL TITLE  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL

I. U. Y., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J.,  
Lorensunhevi, L., Loulsegged, H., Lorado, R. J., Lu, X., Ma, J.,  
Maheshwari, M., Mahindaratne, M., Mahmood, M., Mallory, K., Mangum, A.,  
Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E.,  
Mawhinney, S., McLeod, M. P., McNeill, T. Z., Meenen, E.,  
Milaasviyevic, A., Miner, G., Mnjib, E., Montemayor, J., Moore, S.,  
Morgan, M., Morris, K., Morris, S., Mundasa, M., Murphy, M., Nair, L.,  
Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S.,  
Nwaokwelen, O., Okwunonu, G., Olampunsaogun, A., Pal, S., Parks, K.,  
Pasternak, S., Paul, H., Perez, A., Perez, L., Pflanzkoch, C.,  
Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L.,  
Puzao, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M. A., Reigh, R.,  
Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F.,  
Rivers, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S. J.,  
Sanders, W., Saverly, G., Scherer, S., Scott, G., Shatsman, S., Shen, H.,  
Shetty, J., Shartsbeyn, A., Slasson, I., Sitter, C. D., Smay, D.,  
Sneed, A. J., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J.,  
Steinle, M., Strong, R., Sutton, A., Svatek, A., Taber, P., Taylor, C.,  
Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Umanik, K.,  
Valas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wang, J.,  
Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F.,  
Williams, G., Willison, R., Wlececyk, R., Wooden, H., Worley, K.,  
Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, Y.,  
Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von  
Niederhausern, A., Weiss, R., Smith, D. R., Holt, R. A., Smith, H. O.,  
Weinstock, G. and Gibbs, R. A.

JOURNAL TITLE  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL

Unpublished  
2 (bases 1 to 209701)  
Worley, K.C.  
Direct Submission  
Submitted (19-FEB-2002) Human Genome Sequencing Center, Department  
of Molecular and Human Genetics, Baylor College of Medicine, One  
Baylor Plaza, Houston, TX 77030, USA

RESULT 24				
AC111966/c				
LOCUS	AC111966	209701 bp	DNA	linear
DEFINITION	Rattus norvegicus clone CH230-18S04, ***		SEQUENCING IN PROGRESS	HTG 20-NOV-2002

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
3	(bases 1 to 209701)	Rat Genome Sequencing Consortium.	Submitted (20-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA	On Nov 20, 2002 this sequence version replaced g1:23266189.

ACCESSION	AC111966	GI:25139313
VERSION	AC111966.4	
KEYWORDS	HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_ENRICHED	
SOURCE	Rattus norvegicus (Norway rat)	
ORGANISM	Rattus norvegicus	

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

## REFERENCE

## AUTHORS

1 (bases to 209701)  
Muzny, D., Marie, Metzker, M., Lee, Abramson, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Angiano, D., Anyalebechi, V., Aoyagi, A., Ayodele, L. M., Bacc, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Bernamed, F., Biwalto, K., Blair, J., Blunkburg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Butrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Cessari, H., Center, A., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M. L., Davis, C., Day-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denso, S., Detamco, C., Ding, Y., Dinh, H., Diya, K., Draper, H., Dugan-Roches, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Eugene, C., Evans, C. A., Falls, T., Fan, G., Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P., Fraser, C. M., Gabis, L., Ganta, R., Garcia, A., Garner, T., Garza, M., Gebregeorgis, E., Geer, K., Gill, R., Grady, M., Guerra, M., Guevara, W., Gunaratne, P., Haaland, W., Hamill, C., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Hernandez, R., Hines, S., Hladin, S. L., Hodgson, A., Hogues, M., Hollins, B., Howells, S., Huyls, S., Hume, J., Idlebird, D., Jackson, A., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jollivet, A., Karpach, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovac, C., Kowals, C., Kraft, C. L., Lebnow, H., Lévay, N., Lewis, L., Li, Z., Liu, J.,

Liu, Y., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J.,  
 Lorenzshew, L., Loutsaged, H., Locardo, R.J., Lu, X., Ma, J.,  
 Maheshwari, M., Mahindaratne, M., Mahmood, M., Mallory, K., Mangum, A.,  
 Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E.,  
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 Miska-Jevic, A., Miner, G., Minj, E., Montemayor, J., Moore, S.,  
 Morgan, M., Morris, K., Morris, S., Muidasa, M., Murphy, N.,  
 Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S.,  
 Nwaelele, O., Okwunonu, G., Olampunsaagon, A., Pal, S.,  
 Pasternack, S., Paul, H., Perez, A., Perez, L., Pfankuch, C.,  
 Plapper, F., Polidexter, A., Popovic, D., Prims, E., Pu, L.,  
 Puzo, M., Quiroz, J., Rachlin, E., Reeves, K., Reiter, M.A., Reigh, R.,  
 Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F.,  
 Rivers, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Rutz, S.,  
 Sanders, W., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H.,  
 Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smigs, D.,  
 Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J.,  
 Steinle, M., Strong, R., Sutton, A., Sytek, A., Tabors, P., Taylor, C.,  
 Taylor, T., Thomas, N., Thomas, A., Tingey, A., Tjor, Z.,  
 Valas, R., Vera, V., Villalona, D., Walston, L., Walker, B., Wang, J.,  
 Wang, O., Wang, S., Warren, J., Warren, R., Wei, X., White, F.,  
 Williams, G., Willson, R., Wlecyk, R., Wood, H., Wolley, K.,  
 Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L.,  
 Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von  
 Niederhausen, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O.,  
 Weinstock, G., and Gibbs, R.A.

Direct Submission  
 2 (bases 1 to 209701)  
 Unpublished  
 Morley, K.C.

Direct Submission  
 Submitted (19-FEB-2002) Human Genome Sequencing Center, Department  
 of Molecular and Human Genetics, Baylor College of Medicine, One  
 Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 209701)  
 Rat Genome Sequencing Consortium.

Direct Submission  
 Submitted (20-NOV-2002) Human Genome Sequencing Center, Department  
 of Molecular and Human Genetics, Baylor College of Medicine, One  
 Baylor Plaza, Houston, TX 77030, USA  
 On Nov 20, 2002 this sequence version replaced g1.23266189.

The sequence in this assembly is a combination of BAC based reads  
 and whole genome shotgun sequencing reads assembled using Atlas  
 (<http://www.hgsc.bcm.tmc.edu/projects/atl/>). Each contig described  
 in the feature table below represents a scaffold in the Atlas  
 assembly (a 'contig-scaffold'). Within each contig-scaffold,  
 individual sequence contigs are ordered and oriented, and separate  
 sized gaps filled with Ns to the estimated size. The sequence  
 may extend beyond the ends of the clone and there may be sequence  
 contigs within a contig-scaffold that consist entirely of whole  
 genome shotgun sequence reads. Both end sequences and whole genome  
 shotgun sequence only contigs will be indicated in the feature  
 table.

----- Genome Center -----  
 Center: Baylor College of Medicine  
 Center code: BCM  
 Web site: <http://www.hgsc.bcm.tmc.edu/>  
 Contact: hgsc-help@bcm.tmc.edu  
 ----- Project Information -----  
 Center project name: GOXP  
 Center clone name: CH230-18504  
 ----- Summary Statistics -----  
 Assembly program: Phrap; version 0.990329  
 Consensus quality: 186401 bases at least Q40  
 Consensus quality: 189424 bases at least Q30  
 Consensus quality: 192483 bases at least Q20  
 Estimated insert size: 189615; sum-of-contigs estimation  
 Quality coverage: 6x in Q20 bases; sum-of-contigs estimation

\* NOTE: Estimated insert size may differ from sequence length  
 (see [http://www.hgsc.bcm.tmc.edu/docs/genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html))  
 \* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 1 contigs. Gaps between the contigs



- \* are represented as runs of N. The order of the pieces
- \* is believed to be correct as given, however the sizes
- \* of the gaps between them are based on estimates that have
- \* provided by the submittor.
- \* This sequence will be replaced
- \* by the finished sequence as soon as it is available and
- \* the accession number will be preserved.

1 209701: contig of 209701 bp in length.  
Location/Qualifiers

1..209701

/organism="Rattus norvegicus"

/mol\_type="genomic DNA"

/db\_xref="taxon:10116"

/clone="CH230-18504"

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/note="wgs\_end-extension"

clone\_end:Sp6"

3332..4135

/note="clone\_boundary"

clone\_end:Sp6

end\_sequence:BH266571"

101254..102704

/note="wgs\_contig"

102916..103994

/note="wgs\_contig"

complement(208485..209277)

/note="clone\_boundary"

clone\_end:T7

end\_sequence:BH266569"

56455 a 42541 c 42380 g 52735 t 15590 others

BASE COUNT

ORIGIN

Query Match

Best Local Similarity 66.2% Pred No.32;

Matches 47; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

OY 14 TAACAGTTTAAAGCAGCATTAATAGCTCGCATATGTGATTCATAACAGTTAA 73

DB 105822 TAACAGTTTATTTGATTAATTAACCTCTTTATTTCTGAATGCTCTATAGTCC 105763

OY 74 AACGCTATT 84

DB 105762 AACCTATT 105752

RESULT 25

AC095096/c

LOCUS

DEFINITION

AC095096

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

1 (bases 1 to 252839)

Muzny,D.,Marle,M.,Metzger,M.,Lee,A.,Abramson,S.,Adams,C.,Alder,J.,

Allen,C.,Allen,H.,Alsbrooks,S.,Amlin,A.,Anguliano,D.,

Anyalebechi,V.,Ayoyagi,A.,Ayodeji,M.,Baca,E.,Baden,H.,

Baldwin,D.,Bandaranaik,D.,Barber,M.,Barnstead,M.,Benahmed,F.,

Biswal,K.,Blair,J.,Blankenburg,K.,Blyth,P.,Brown,M.,

Bryant,N.,Buhay,C.,Burch,P.,Buttelli,K.,Calderton,E.,

Caldenas,V.,Carter,K.,Cavazos,I.,Cesar,H.,Center,A.,

Chacko,J.,Chavez,D.,Chen,G.,Chen,R.,Chen,Y.,Chen,Z.,Chu,J.,

Chavland,C.,Cockrell,R.,Cox,C.,Coyle,M.,Cree,A.,D'Souza,L.,

Davila,M.L.,Davis,C.,Davy-Carroll,L.,De Anda,C.,Dederich,D.,

Delgado,O.,Denson,S.,Deramo,C.,Ding,Y.,Dinh,H.,Diya,K.,

Egan,A.,Escotto,M.,Eugene,C.,Evans,C.A.,Falls,T.,Fan,G.,  
Fernandez,S.,Finley,M.,Flagg,N.,Forbes,L.,Foster,M.,Foster,P.,  
Fraser,C.M.,Gabisi,A.,Ganta,R.,Garcia,A.,Garner,T.,Garza,M.,  
Gebregorgis,E.,Geer,K.,Gill,R.,Grady,M.,Guerra,W.,Guevara,W.,  
Gunaratne,P.,Haaland,W.,Hamil,C.,Hamilton,C.,Hamilton,K.,  
Harvey,Y.,Havlik,P.,Hawes,A.,Henderson,N.,Hernandez,J.,  
Hernandez,R.,Hines,S.,Hladun,S.L.,Hodgson,A.,Hogues,M.,  
Hollins,B.,Howells,S.,Hulik,S.,Hume,J.,Idlebird,D.,Jackson,A.,  
Jackson,L.,Jacob,L.,Jiang,H.,Johnson,B.,Johnson,R.,Jolivet,A.,  
Karpathy,S.,Kelly,S.,Kelly,S.,Khan,Z.,King,L.,Kovar,C.,  
Kowis,C.,Kraft,C.L.,Ledow,H.,Levan,J.,Lewis,L.,Li,Z.,Liu,J.,  
Liu,J.,Liu,W.,Liu,Y.,London,P.,Longacre,S.,Lopez,J.,  
Lorenshewa,L.,Lounseged,H.,Lozado,R.J.,Lu,X.,Ma,J.,  
Maheshwari,M.,Mahindaratne,M.,Maimoud,M.,Mallory,K.,Mangum,A.,  
Mangum,B.,Mapua,P.,Martin,K.,Martin,R.,Martinez,E.,  
Mawhinney,S.,McLeod,M.P.,McNeill,T.Z.,Meenen,E.,  
Miosavljovic,A.,Miner,G.,Minja,E.,Montemayor,J.,Moore,S.,  
Morgan,M.,Morris,K.,Morris,S.,Munidas,M.,Murphy,M.,Nair,L.,  
Nankervis,C.,Neal,D.,Newton,N.,Nguyen,N.,Norris,S.,  
Nwackeleneh,O.,Okunolu,G.,Olarnpungoon,A.,Pal,S.,Parks,K.,  
Pasternak,S.,Paul,H.,Perez,A.,Perez,L.,Pfankoch,C.,  
Plopper,F.,Poindexter,A.,Popovic,D.,Prims,E.,Pu,L.,T.,  
Puzo,M.,Quiroz,J.,Rachlin,E.,Reeves,K.,Regier,M.A.,Reigh,R.,  
Reilly,B.,Reilly,M.,Ren,Y.,Reuter,M.,Richards,S.,Riggs,F.,  
Rives,C.,Rodkey,T.,Rojas,A.,Rose,M.,Rose,R.,Rulz,S.J.,  
Sanders,M.,Savery,G.,Scherer,S.,Scott,G.,Shatsman,S.,Shen,H.,  
Shetty,J.,Shvartsbeyn,A.,Sison,I.,Slitter,C.D.,Smajls,D.,  
Sneed,A.,Sodergren,E.,Song,X.-Z.,Sorelle,R.,Sosa,J.,  
Steinle,M.,Strong,R.,Sutton,A.,Svatek,A.,Taber,P.,Taylor,C.,  
Taylor,T.,Thomas,N.,Thomas,S.,Tingey,A.,Trijos,Z.,Usmani,K.,  
Valas,R.,Vera,V.,Villasana,D.,Waldron,L.,Walker,B.,Wang,J.,  
Wang,Q.,Wang,S.,Warren,J.,Warren,R.,Wel,X.,White,F.,  
Williams,G.,Willson,R.,Wleczyk,R.,Wooden,H.,Worley,K.,  
Wright,D.,Wright,R.,Wu,J.,Yakub,S.,Yen,J.,Yoon,L.,Yoon,V.,  
Yu,F.,Zhang,J.,Zhou,J.,Zhou,X.,Zhao,S.,Zimm,D.,von  
Wiederhausen,A.,Weiss,R.,Smith,D.R.,Holt,R.A.,Smith,H.O.,  
Wienstock,G.,and Gibbs,R.A.

#### TITLE

Direct Submission

Unpublished

2 (bases 1 to 252839)

Worley,K.C.

Direct Submission

Submitted (16-SEP-2001) Human Genome Sequencing Center, Department

of Molecular and Human Genetics, Baylor College of Medicine, One

Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 252839)

Rat Genome Sequencing Consortium.

Direct Submission

Submitted (09-MAY-2003) Human Genome Sequencing Center, Department

of Molecular and Human Genetics, Baylor College of Medicine, One

Baylor Plaza, Houston, TX 77030, USA

On May 9, 2003 this sequence version replaced gi:24818178.

The sequence in this assembly is a combination of BAC based reads

and whole genome shotgun sequencing reads assembled using Atlas

(http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described

in the feature table below represents a scaffold in the Atlas

assembly (a 'contig-scaffold'). Within each contig-scaffold,

individual sequence contigs are oriented and separated

by sized gaps filled with Ns to the estimated size. The sequence

may extend beyond the ends of the clone and there may be sequence

contigs within a contig-scaffold that consist entirely of whole

genome shotgun sequence reads. Both end sequences and whole genome

shotgun sequence only contigs will be indicated in the feature

table.

#### COMMENT

Genome Center

Center: Baylor College of Medicine

Center code: BCM

Web site: http://www.hgsc.bcm.tmc.edu/

Contact: hgsc-help@bcm.tmc.edu

Project Information

Center project name: GC1H

Center clone name: CH230-7G9

Summary Statistics







In the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

## ----- Genome Center

Center: Baylor College of Medicine  
Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>  
Contact: hgsc-help@bcm.tmc.edu

## ----- Project Information

Center project name: GYU  
Center clone name: CH230-74A9

## ----- Summary Statistics

Assembly program: Phrap; version 0.990329  
Consensus quality: 233743 bases at least Q40  
Consensus quality: 237630 bases at least Q30  
Consensus quality: 239718 bases at least Q20  
Estimated insert size: 239635; sum-of-contigs estimation  
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation

\* NOTE: Estimated insert size may differ from sequence length  
\* (see [http://www.hgsc.bcm.tmc.edu/docs/Genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)).  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 4 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

\* 1 257713: contig of 257713 bp in length  
\* 257714 257813: gap of unknown length  
\* 257814 258986: contig of 1183 bp in length  
\* 258987 259086: gap of unknown length  
\* 259087 261187: contig of 2091 bp in length  
\* 261188 261287: gap of unknown length  
\* 261288 263259: contig of 1972 bp in length.

## FEATURES

Location/Qualifiers

1..263259

/organism="Homo sapiens"

/mol\_type="genomic DNA"

/db\_xref="taxon:9606"

/clone="CH230-74A9"

1..1068

/note="wgs\_contig"

2206..5188

/note="wgs\_contig"

256153..257713

/note="wgs\_contig"

BASE COUNT 69680 a 54257 c 54754 g 62449 t 22119 others

## ORIGIN

Query Match 31.7%; Score 32.6; DB 2; Length 263259;

Best Local Similarity 60.9%; Pred. No. 31;

Matches 53; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 15 AACGTTTAAATGACACATTAAAGCTCCGCAATGATGCAATTCATACAGTAAAA 74

DB 105112 AACGGTTTAAATGACACATTAAAGCTCCGCAATGATGCAATTCATACAGTAAAA 105053

QY 75 AACGTTTAAATGACACATTAAAGCTCCGCAATGATGCAATTCATACAGTAAAA 101

DB 105052 ATCTGATTTCCATGCTCATTCCTA 105026

RESULT 28  
AP004386/c 159598 bp DNA linear PRI 02-FEB-2002  
LOCUS AP004386

DEFINITION Homo sapiens genomic DNA, chromosome 8q23, clone:KB1154F4.

AP004386

AP004386.2 GI:18479066

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens

Homo sapiens

Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE

1 Shimizu, N. and Asakawa, S.

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

Submitted (30-NOV-2001) Nobuyoshi Shimizu, Keio University, School

of Medicine, Molecular Biology, 35 Shinanomachi, Shinjuku-ku, Tokyo

160-8582, Japan (E-mail: nshimizu@med.keio.ac.jp,

Tel: 81-3-3351-2370, Fax: 81-3-3351-2370)

On Feb 2, 2002 this sequence version replaced gi:17298203.

COMMENT

FEATURES

Source

1..159598

/organism="Homo sapiens"

/mol\_type="genomic DNA"

/db\_xref="taxon:9606"

/chromosome="8"

/map="8q23"

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/cell\_line="FEB 14 - 14"

/cell\_type="pre-pro-B cell"

/clone\_lib="Keio BAC library"

complement(5..1942)

/evidence=not\_experimental

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complement(1984..2203)

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/rpt\_family="LMCb"

2204..2230

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2230..2255

/evidence=not\_experimental

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complement(2231..3770)

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complement(5011..5364)

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5411..6176

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6218..6570

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complement(9511..9633)

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10350..10386

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13323..13362

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13636..13660

/evidence=not\_experimental

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repeat_region 17118..17156
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/rpt_family="CT-rich"
repeat_region 17176..17619
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repeat_region 17792..17934
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repeat_region 19682..19850
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/rpt_family="LIP1"
repeat_region complement(20360..20405)
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repeat_region 28031..28055
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repeat_region 30873..30893

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repeat_region complement(36585..36717)
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Query Match 31.5%; Score 32.4; DB 9; Length 159598;
Best Local Similarity 62.2%; Pred. No. 38;
Matches 51; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

OY 5 TGACGGAATAACGATTAAATGACGACGATTAAGCTCCGTGCATATGTGAATGCTAATA 64
DB 13823 TCACAGAGATGTCACATCCACAGCAAGATTTGCTGTTCATCTTTAGCTTGC 138174
OY 65 CAGTTAAATAAACGATTTCC 86
DB 138173 CACTTAACACTACATTTTCC 138152

RESULT 29
AL954648 167153 bp DNA linear HTG 12-MAR-2003
LOCUS AL954648
DEFINITION Dario rerio clone CH211-245P24, *** SEQUENCING IN PROGRESS ***, 2
ACCESSION AL954648
```

RESULT	30
AC090142	197877 bp DNA linear PRI 27-MAR-2002
LOCUS	Homo sapiens chromosome 8, clone RP11-200A13, complete sequence.
DEFINITION	AC090142
ACCESSION	AC090142
VERSION	AC090142.3
KEYWORDS	GI:19683145
ORGANISM	HTE.
SOURCE	Homo sapiens (human)
REFERENCE	Homo sapiens
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE	1 (bases 1 to 197877)
JOURNAL	Bliren, B., Linton, L., Nusbaum, C. and Lander, E.
REFERENCE	Homo sapiens chromosome 8, clone RP11-200A13
AUTHORS	Unpublished
	2 (bases 1 to 197877)
	Bliren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, S., Barna, N., Bastien, V., Boguslavsky, L., Boukhalter, B., Brown, A., Camarata, J., Campolano, A., Choepel, Y., Colangelo, M., Collins, S., Collimore, A., Cooke, P., DeArrellano, K., Dewar, K., Diaz, J. S., Dodge, S., Faro, S., Ferreira, P., Fitzhugh, W., Gage, D., Galaan, J., Gardyna, S., Goyette, S., Goyette, M., Graham, L., Grand-Pierre, R., Hagos, B., Hearford, A., Horton, L., Huine, W., Iliev, I., Johnson, R., Jones, C., Karatas, A., Lacroque, K., Lamazares, R., Landers, T., Lehoccky, J., Levine, R., Liu, G., Maclean, C., MacDonald, P., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., MCPheeters, R., Meldrim, J., Menus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Norbu, C., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Plunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, N., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupack, R., Seaman, S., Severy, P., Sounguez, C., Spencer, B., Strange-Thomann, N., Stojanovic, N., Straus, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Travets, M., Travis, N., Triglio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W., J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
TITLE	Direct Submission
JOURNAL	Submitted (17-FEB-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
REFERENCE	3 (bases 1 to 197877)
AUTHORS	Bliren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavsky, L., Boukhalter, B., Brown, A., Camarata, J., Campolano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collimore, A., Cook, A., Cooke, P., DeArrellano, K., Dewar, K., Diaz, J. S., Dodge, S., Faro, S., Ferreira, P., Fitzhugh, W., Gage, D., Galaan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Huine, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Lacroque, K., Lamazares, R., Landers, T., Lehoccky, J., Levine, R., Lindblad-Toh, K., Liu, G., Maclean, C., MacDonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrim, J., Menus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Plunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Roman, J., Rieback, N., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupack, R., Seaman, S., Severy, P., Spencer, B., Strange-Thomann, N., Stojanovic, N., Straus, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travets, M., Travis, N., Triglio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W., J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
TITLE	Direct Submission
JOURNAL	Submitted (22-MAR-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
REFERENCE	4 (bases 1 to 197877)
AUTHORS	Bliren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavsky, L., Boukhalter, B., Brown, A., Camarata, J., Campolano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collimore, A.,

Faro, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hags, B., Horton, L., Huime, W., Iliev, I., Johnson, R., Jones, C., Kamel, A., Karatas, A., Kellis, C., LaRoque, K., Lamazares, R., Landers, T., Lehoczy, J., Levine, R., Lindblad-Toh, K., Liu, G., Maclean, C., MacDonald, P., Major, J., Margulis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Melgrim, J., Menes, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phukhang, P., Pierre, N., Pollara, V., Raymond, C., Rella, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, D., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupack, R., Seaman, S., Severy, P., Spencer, B., Stange-Rhmann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Submitted (27-MAR-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA  
On Mar 22, 2002 this sequence version replaced g1:14150949.  
All repeats were identified using RepeatMasker:  
Smit, A.F.A. & Green, P. (1996-1997)  
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center  
Center: Whitehead Institute/ MIT Center for Genome Research  
Center code: WIBR  
Web site: <http://www-seq.wi.mit.edu>  
Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)  
----- Project Information  
Center project name: L11673  
Center clone name: 200\_A\_13

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	repeat_region	13383..13444 /rpt_family="(MERSA"
	repeat_region	13692..13995 /rpt_family="(CA)n"
	repeat_region	complement(14392..14570) /rpt_family="(AluSg/x"
	repeat_region	14985..15149 /rpt_family="(MIR"
	repeat_region	15463..15483 /rpt_family="(AT_rich"
	repeat_region	15935..15961 /rpt_family="(AT_rich"
	repeat_region	16098..16146 /rpt_family="(TGA)n"
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	unsure	complement(16653..16659) /note="<30 qual SNGL region"
	unsure	complement(17859..17864) /note="<30 qual SNGL region"
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	repeat_region	20955..21016 /rpt_family="(TG)n"
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	repeat_region	23357..23400 /rpt_family="(CATATA)n"
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Query Match 31.5% Score 32.4: DB 9: Length 197877;  
Best Local Similarity 62.2% Pred. No. 37;  
Matches 51; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

OY	5	TGACTGCAATAACAGTTTAATGACAGCATTAATAGCTCCGATATGTGAATGCTATA 64
DB	42237	TCACAGAGATGTCAGTTCCATGACAGCAAGATTTGCTTTCATCTTTTACCTCTG 42236
OY	65	CAGTTAAAAAAGCGTATTC 86
DB	42297	CACTTAAACATCAATTTTCC 42318

RESULT 31  
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LOCUS AC069127 198176 bp DNA linear HTG 01-SEP-2000  
 DEFINITION Homo sapiens chromosome 8 clone RP11-200A13, WORKING DRAFT  
 ACCESSION AC069127  
 VERSION AC069127.1 GI:7923969  
 KEYWORDS HTG; HTGS\_PHASE1; HTGS\_DRAFT.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 198176)  
 TITLE Waterston,R.H.  
 JOURNAL The sequence of Homo sapiens clone  
 REFERENCE 2 (bases 1 to 198176)  
 TITLE Waterston,R.H.  
 JOURNAL Submitted (18-MAY-2000) Genome Sequencing Center, Washington  
 DIRECT SUBMISSION University School of Medicine, 4444 Forest Park Parkway, St. Louis,  
 MO 63108, USA  
 COMMENT  
 ----- Genome Center -----  
 Center: Washington University Genome Sequencing Center  
 Center code: WUGSC  
 Web site: http://genome.wustl.edu/gsc/index.shtml  
 ----- Project Information -----  
 Center project name: H\_NH0200A13  
 ----- Summary Statistics -----  
 Sequencing vector: plasmid; 100%  
 Chemistry: Dye-terminator Big Dye; 0% of reads  
 Assembly program: Phrap; version 0.990319  
 Consensus quality: 190387 bases at least Q40  
 Consensus quality: 193248 bases at least Q30  
 Consensus quality: 194812 bases at least Q20  
 Insert size: 188000; agarose-fp  
 Insert size: 196776; sum-of-contigs  
 Quality coverage: 4.45 in Q20 bases; sum-of-contigs  
 Quality coverage: 4.27 in Q20 bases; sum-of-contigs  
 ----- NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 15 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.  
 1 1104: contig of 1104 bp in length  
 \* 1105 1204: gap of unknown length  
 \* 1205 2731: contig of 1527 bp in length  
 \* 2732 2831: gap of unknown length  
 \* 2832 7084: contig of 4253 bp in length  
 \* 7085 7184: gap of unknown length  
 \* 7185 10684: contig of 3500 bp in length  
 \* 10685 10784: gap of unknown length  
 \* 10785 16048: contig of 5264 bp in length  
 \* 16049 16148: gap of unknown length  
 \* 16149 21738: contig of 5590 bp in length  
 \* 21739 21838: gap of unknown length  
 \* 21839 27347: contig of 5509 bp in length  
 \* 27348 27447: gap of unknown length  
 \* 27448 33889: contig of 6442 bp in length  
 \* 33890 33989: gap of unknown length  
 \* 33990 50271: contig of 16282 bp in length  
 \* 50272 50371: gap of unknown length  
 \* 50372 66236: contig of 15865 bp in length  
 \* 66237 66336: gap of unknown length  
 \* 66337 85017: contig of 18681 bp in length  
 \* 85018 85117: gap of unknown length  
 \* 85118 103112: contig of 17995 bp in length  
 \* 103113 103212: gap of unknown length

FEATURES  
 source  
 \* 103213 132684: contig of 29472 bp in length  
 \* 132685 132784: gap of unknown length  
 \* 132785 161923: contig of 29139 bp in length  
 \* 161924 162023: gap of unknown length  
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 162024. 198176  
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 Best Local Similarity 62.2% Pred. No. 37;  
 Matches 51; Conservative 0; Mismatches 31; Indels 0; Gaps 0;  
 Oy 5 TGAAGTAAATACGTTAATGACGATTAATGCTCGCATATGTAATGCTATA 64  
 | ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
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 Oy 65 CAGTTAAAAAAGCGATTTC 86  
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 RESULT 32  
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 LOCUS AL954337  
 DEFINITION Danio rerio clone CH211-223J10, \*\*\* SEQUENCING IN PROGRESS \*\*\*, 2  
 ACCESSION AL954337  
 VERSION AL954337.7 GI:29786487  
 KEYWORDS HTG; HTGS\_PHASE1; HTGS\_ACTIVEFIN; HTGS\_DRAFT; HTGS\_FULLTOP.  
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 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii: Neopterygii: Teleostei: Ostariophysi:  
Cypriniformes: Cyprinidae: Danio.  
1 (bases 1 to 205394)  
Kay, M.  
Direct Submission  
Submitted (02-MAY-2003) Wellcome Trust Sanger Institute, Hinxton,  
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:  
zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk  
On Apr 10, 2003 this sequence version replaced g1:29561800.  
----- Genome Center  
Center: Wellcome Trust Sanger Institute  
Center code: SC  
Web site: <http://www.sanger.ac.uk>  
Contact: zfish-help@sanger.ac.uk  
----- Project Information  
Center project name: zc223j10  
----- Summary Statistics  
Assembly program: XGAP4; version 4.5  
Chemistry: Dye-terminator; 99% of reads  
Chemistry: Dye-primer Big Dye; 0% of reads  
Consensus quality: 205262 bases at least Q40  
Consensus quality: 205273 bases at least Q30  
Consensus quality: 205282 bases at least Q20  
Insert size: 205294; sum-of-contigs  
Insert size: 207449; 7.7% error; agarose-fp  
Quality coverage: 10.18x in Q20 bases; sum-of-contigs Quality  
coverage: 10.49x in Q20 bases; agarose-fp  
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\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 2 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.  
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\* 4047 4146: gap of 100 bp  
\* 4147 205394: contig of 201248 bp in length.  
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ORIGIN  
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Best Local Similarity 62.2%; Pred. No. 37;  
Matches 51; Conservative 0; Mismatches 31; Indels 0; Gaps 0;  
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DB 194930 GTTCTGTGGCTCTCATCTAGCA 194909  
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LOCUS AC021546 207756 bp DNA linear PRI 29-JUN-2001

DEFINITION Homo sapiens chromosome 8, clone RP11-57407, complete sequence.  
AC021546  
AC021546 GI:14140331  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Homo sapiens (human)  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
RECORD  
AUTHORS  
Boguslavsky, L., Boukhalter, B., Brown, A., Burkett, G., Castle, A.,  
Chopell, Y., Colangelo, M., Collins, S., Collamore, A., Cooke, P.,  
Ferreira, P., Fitzhugh, W., Forrest, C., Gage, D., Galagan, J.,  
Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L.,  
Howard, J. C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J.,  
Lander, E., Lechoczy, J., Levine, R., Liu, C., Liu, G., Locke, K.,  
Macdonald, P., Margus, N., McEwan, P., McGuirk, A., McKernan, K.,  
McPheeters, R., Meldrum, J., Menus, L., Morrow, J., Naylor, J.,  
Norman, C. H., O'Connor, T., O'Donnell, P., Oliver, T. M., Peterson, K.,  
Pierre, N., Pisan, C., Pollara, V., Raymond, C., Riley, R., Rotman, D.,  
Roy, A., Santos, R., Severy, P., Spencer, B., Stange-Thomann, N.,  
Stojanovic, N., Subramanian, A., Talamas, J., Testaye, S., Theodore, J.,  
Tirrell, A., Vassiliev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W. J.,  
Zimmer, A., and Zody, M.  
Direct Submission  
Submitted (16-JAN-2000) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
3 (bases 1 to 207756)  
TITLE  
JOURNAL  
RECORD  
AUTHORS  
Birken, B., Linton, L., Nusbaum, C., Lander, E., Allen, N.,  
Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F.,  
Boguslavsky, L., Boukhalter, B., Brown, A., Burkett, G., Castle, A.,  
Chopell, Y., Colangelo, M., Collins, S., Collamore, A., Cooke, P.,  
Ferreira, P., Fitzhugh, W., Forrest, C., Gage, D., Galagan, J.,  
Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L.,  
Howard, J. C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J.,  
Lander, E., Lechoczy, J., Levine, R., Liu, C., Liu, G., Locke, K.,  
Macdonald, P., Margus, N., McEwan, P., McGuirk, A., McKernan, K.,  
McPheeters, R., Meldrum, J., Menus, L., Morrow, J., Naylor, J.,  
Norman, C. H., O'Connor, T., O'Donnell, P., Oliver, T. M., Peterson, K.,  
Pierre, N., Pisan, C., Pollara, V., Raymond, C., Riley, R., Rotman, D.,  
Roy, A., Santos, R., Severy, P., Spencer, B., Stange-Thomann, N.,  
Stojanovic, N., Subramanian, A., Talamas, J., Testaye, S., Theodore, J.,  
Tirrell, A., Vassiliev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W. J.,  
Zimmer, A., and Zody, M.  
Direct Submission  
Submitted (29-JUN-2001) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
On May 17, 2001 this sequence version replaced g1:13518209.  
All repeats were identified using RepeatMasker:  
Smit, A.F.A. & Green, P. (1996-1997)  
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>  
----- Genome Center  
Center: Whitehead Institute/ MIT Center for Genome Research  
Center code: W1BR  
Web site: <http://www-seq.wi.mit.edu>  
Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)  
----- Project Information  
Center project name: L5615  
Center clone name: 574\_O\_7  
----- Location/Qualifiers



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7510..8455
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repeat_region
complement(9622..10018)
/rpt_family="L1MB4"
10040..10111
/rpt_family="L2"
11845..11895
/rpt_family="MLT1I"
12535..12614
/rpt_family="AT_rich"
complement(15747..16082)
/rpt_family="Alusx"
16212..16597
/rpt_family="L2"
19254..19325
/rpt_family="(TATATG)n"
complement(19374..19685)
/rpt_family="AluSp"
complement(19848..20376)
/rpt_family="L1ME3"
20575..20610
/rpt_family="AT_rich"
complement(20683..21058)
/rpt_family="L1ME3"
21401..21401
/rpt_family="L2"
complement(21437..22069)
/rpt_family="L1PA16"
22070..22636
/rpt_family="L1P"
22782..22852
/rpt_family="(TCTA)n"
complement(22974..24021)
/rpt_family="MER11C"
24763..24947
/rpt_family="LTR33"
25200..25355
/rpt_family="(TA)n"
26339..26377
repeat_region

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/rpt_family="AT_rich"
26378..26751
/rpt_family="L1ME1"
26898..27087
/rpt_family="L1MEC"
27419..27517
/rpt_family="L1MEC"
27641..27786
/rpt_family="L1MEC"
27865..28587
/rpt_family="L1MEC"
28588..28858
/rpt_family="AluSg"
28859..29091
/rpt_family="L1MEC"
complement(29092..30048)
/rpt_family="L1PA11"
30049..30653
/rpt_family="L1MEC"
30665..30849
/rpt_family="L1MDa"
30905..31089
/rpt_family="L1MCB"
31108..31560
/rpt_family="L1MCB"
31600..31625
/rpt_family="(TG)n"
31613..31615
/note="single clone coverage"
31621..31632
/note="<30 qual SNGL region"
31646..31681
/note="<30 qual SNGL region"
31651..31783
/rpt_family="L1M1"
31699..31704
/note="<30 qual SNGL region"
complement(31797..32731)
/rpt_family="L1M1"
32730..32942
/rpt_family="L1M1"
32958..33397
/rpt_family="L1MCB"
33398..33596
/rpt_family="rigger1"
complement(33597..35907)
/rpt_family="AluY"
35908..36103
/rpt_family="rigger1"
36104..36250
/rpt_family="L1MCB"
36251..36553
/rpt_family="AluSc"

```

Query Match 31.5%: Score 32.4: DB 9: Length 207756;  
 Best Local Similarity 62.2%: Pred. No. 37;  
 Matches 51: Conservative 0: Mismatches 31: Indels 0: Gaps 0:

```

OY 5 TGACTGGAATACAGTTTAATAGACAGCATATAGCTCCATATGTGAATTGCTATATA 64
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 162975 TCACTAGATGTCACTGCTCCAGACAGCATTTTGTCTTTCATCTTTTACCTTCTG 163034
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 65 CAGTTAAAAAAGCGATTTCG 86
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 163035 CACTTTAAACTACATTTTTCG 163056
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

RESULT 34  
 AC125433/c AC125433 57810 bp DNA linear HTG 26-JUN-2002  
 LOCUS Homo sapiens chromosome 11 clone RP11-32218 map 11, LOW-PASS  
 DEFINITION  
 SEQUENCE SAMPLING.  
 ACCESSION AC125433

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VERSION      AC125433.1 GI:21591978
KEYWORDS     HTG: HTGS_PHASE0.
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
REFERENCE    Mammalia: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
AUTHORS      1 (bases 1 to 37810)
TITLE        Birren, B., Nusbaum, C. and Lander, E.
JOURNAL      Homo sapiens chromosome 11, clone RP11-322L8
REFERENCE    Unpublished
AUTHORS      2 (bases 1 to 57810)
REFERENCE    Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S.,
AUTHORS      Barra, N., Bastien, V., Bloom, F., Boguslavsky, L., Bonkhgatter, B.,
AUTHORS      Camarata, J., Chang, J., Chazaro, R., Choepel, Y., Collymore, A.,
AUTHORS      Cook, A., Cooke, P., Dearrellano, R., Dewar, K., Diaz, J. S., Dodge, S.,
AUTHORS      Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J.,
AUTHORS      Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B.,
AUTHORS      Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A.,
AUTHORS      Karatas, A., Kellis, C., Landers, T., Levine, R., Lindblad-Toh, K.,
AUTHORS      Liu, G., Maclean, C., MacDonald, P., Major, J., Matthews, C.,
AUTHORS      McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V.,
AUTHORS      Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C. H.,
AUTHORS      O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K.,
AUTHORS      Phukhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P.,
AUTHORS      Roman, J., Roy, A., Schauer, S., Schnupack, R., Seaman, S., Severy, P.,
AUTHORS      Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J.,
AUTHORS      Testaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H.,
AUTHORS      Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J.,
AUTHORS      Zemek, L., Zimmer, A. and Zody, M.
COMMENT      Submitted (26-JUN-2002) Whitehead Institute/MIT Center for Genome
COMMENT      Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT      All repeats were identified using RepeatMasker:
COMMENT      Smit, A.F.A. & Green, P. (1996,1997)
COMMENT      http://ftp.genome.washington.edu/RM/RepeatMasker.html
COMMENT      ----- Genome Center
COMMENT      Center: Whitehead Institute/ MIT Center for Genome Research
COMMENT      Web site: http://www-seq.wi.mit.edu
COMMENT      Contact: sequence_submissions@genome.wi.mit.edu
COMMENT      ----- Project Information
COMMENT      Center project name: L27569
COMMENT      Center clone name: 322_L_8
COMMENT      -----
* NOTE: This record contains 69 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.
*
* 1 701: contig of 701 bp in length
* 2 801: gap of 100 bp
* 702 801: gap of 100 bp
* 802 1571: contig of 770 bp in length
* 1572 1671: gap of 100 bp
* 1672 2436: contig of 765 bp in length
* 2437 2537: gap of 100 bp
* 2537 3244: contig of 708 bp in length
* 3245 3344: gap of 100 bp
* 3344 4072: contig of 728 bp in length
* 4073 4173: gap of 100 bp
* 4173 4921: contig of 749 bp in length
* 4922 5021: gap of 100 bp
* 5022 5787: contig of 766 bp in length
* 5788 5887: gap of 100 bp
* 5888 6642: contig of 755 bp in length
* 6643 6742: gap of 100 bp
* 6743 7507: contig of 765 bp in length
* 7508 7607: gap of 100 bp
*
* 7608 8309: contig of 702 bp in length
* 8310 8409: gap of 100 bp
* 8410 9184: contig of 775 bp in length
* 9185 9284: gap of 100 bp
* 9285 10041: contig of 757 bp in length
* 10042 10141: gap of 100 bp
* 10142 10887: contig of 746 bp in length
* 10888 10987: gap of 100 bp
* 10988 11723: contig of 736 bp in length
* 11724 11823: gap of 100 bp
* 11824 12560: contig of 737 bp in length
* 12561 12661: gap of 100 bp
* 12661 13407: contig of 747 bp in length
* 13408 13507: gap of 100 bp
* 13508 14240: contig of 733 bp in length
* 14241 14340: gap of 100 bp
* 14341 15029: contig of 689 bp in length
* 15030 15129: gap of 100 bp
* 15130 15893: contig of 764 bp in length
* 15894 15993: gap of 100 bp
* 15994 16747: contig of 754 bp in length
* 16748 16847: gap of 100 bp
* 16848 17600: contig of 753 bp in length
* 17601 17700: gap of 100 bp
* 17701 18424: contig of 724 bp in length
* 18425 18524: gap of 100 bp
* 18525 19241: contig of 717 bp in length
* 19242 19341: gap of 100 bp
* 19342 20080: contig of 739 bp in length
* 20081 20180: gap of 100 bp
* 20181 20907: contig of 727 bp in length
* 20908 21007: gap of 100 bp
* 21008 21767: contig of 760 bp in length
* 21768 21867: gap of 100 bp
* 21868 22594: contig of 727 bp in length
* 22595 22694: gap of 100 bp
* 22695 23454: contig of 760 bp in length
* 23455 23554: gap of 100 bp
* 23555 24315: contig of 761 bp in length
* 24316 24415: gap of 100 bp
* 24416 25179: contig of 764 bp in length
* 25180 25279: gap of 100 bp
* 25280 26030: contig of 751 bp in length
* 26031 26130: gap of 100 bp
* 26131 26876: contig of 746 bp in length
* 26877 26976: gap of 100 bp
* 26977 27730: contig of 754 bp in length
* 27731 27830: gap of 100 bp
* 27831 28582: contig of 752 bp in length
* 28583 28682: gap of 100 bp
* 28683 29438: contig of 756 bp in length
* 29439 29538: gap of 100 bp
* 29539 30303: contig of 765 bp in length
* 30304 30403: gap of 100 bp
* 30404 31087: contig of 684 bp in length
* 31088 31187: gap of 100 bp
* 31188 31950: contig of 763 bp in length
* 31951 32050: gap of 100 bp
* 32051 32799: contig of 749 bp in length
* 32800 32899: gap of 100 bp
* 32900 33649: contig of 750 bp in length
* 33650 33749: gap of 100 bp
* 33750 34462: contig of 713 bp in length
* 34463 34562: gap of 100 bp
* 34563 35306: contig of 744 bp in length
* 35307 35406: gap of 100 bp
* 35407 36149: contig of 743 bp in length
* 36150 36249: gap of 100 bp
* 36250 37003: contig of 754 bp in length
* 37004 37103: gap of 100 bp
* 37104 37872: contig of 769 bp in length
* 37873 37972: gap of 100 bp
* 37973 38703: contig of 731 bp in length

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*      38704      38803: gap of 100 bp
*      38804      39565: contig of 762 bp in length
*      39566      39666: gap of 100 bp
*      39666      40426: contig of 761 bp in length
*      40427      40526: gap of 100 bp
*      40527      41264: contig of 738 bp in length
*      41265      41364: gap of 100 bp
*      41365      42088: contig of 724 bp in length
*      42089      42188: gap of 100 bp
*      42189      42924: contig of 736 bp in length
*      42925      43024: gap of 100 bp
*      43025      43751: contig of 727 bp in length
*      43752      43851: gap of 100 bp
*      43852      44616: contig of 765 bp in length
*      44617      44716: gap of 100 bp
*      44717      45476: contig of 760 bp in length
*      45477      45576: gap of 100 bp
*      45577      46341: contig of 765 bp in length
*      46342      46441: gap of 100 bp
*      46442      47113: contig of 672 bp in length
*      47114      47213: gap of 100 bp
*      47214      47919: contig of 706 bp in length
*      47920      48019: gap of 100 bp
*      48020      48785: contig of 766 bp in length
*      48786      48885: gap of 100 bp
*      48886      49563: contig of 684 bp in length
*      49570      49669: gap of 100 bp
*      49670      50374: contig of 705 bp in length
*      50375      50474: gap of 100 bp
*      50475      51197: contig of 723 bp in length
*      51198      51297: gap of 100 bp
*      51298      52033: contig of 736 bp in length
*      52034      52133: gap of 100 bp
*      52134      52895: contig of 762 bp in length
*      52896      52995: gap of 100 bp
*      52996      53697: contig of 702 bp in length
*      53698      53797: gap of 100 bp
*      53798      54446: contig of 649 bp in length
*      54447      54546: gap of 100 bp
*      54547      55284: contig of 738 bp in length
*      55285      55384: gap of 100 bp
*      55385      56119: contig of 735 bp in length
*      56120      56219: gap of 100 bp
*      56220      56968: contig of 750 bp in length
*      56970      57069: gap of 100 bp
*      57070      57810: contig of 741 bp in length.

```

```

FEATURES
  source
    1..57810
      /organism="Homo sapiens"
      /mol_type="genomic DNA"

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Query Match      31.1%; Score 32; DB 2; Length 57810;
Best Local Similarity 58.3%; Pred. No. 55;
Matches 56; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

```

```

Oy      3      AGTCACCTGAATTAACATTTAATGACAGCATTAATAGCTCTCGATATGTAATGCTAA 62
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      14752  AGTAGCTGGACACACAGCATGTCACACTCCTACATATGTTTTTAAATTTTAA 14693
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Oy      63      TACAGTTAAAAAACGTAATTCCTCGTCTGATC 98
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      14692  TAGAGATGAGGTCTCATTAATTTTGGCCAGGCTGATC 14657
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

```

RESULT 35
AC104655/c      AC104655      95616 bp      DNA      Linear      PRI 21-FEB-2002
LOCUS
DEFINITION      Homo sapiens BAC clone RP11-383P6 from 2, complete sequence.
ACCESSION      AC104655
VERSION      AC104655.4      GI:18482325
KEYWORDS      HTG.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens

```

```

REFERENCE
AUTHORS      Sulston, J.E. and Waterston, R.
TITLE      Toward a complete human genome sequence
JOURNAL      Genome Res. 8 (11), 1097-1108 (1998)
MEDLINE      99063792
PUBMED      9847074
REFERENCE
AUTHORS      Tomlinson, C. and Cotton, M.
TITLE      The sequence of Homo sapiens BAC clone RP11-383P6
JOURNAL      Unpublished (2001)
REFERENCE
AUTHORS      Waterston, R.H.
TITLE      Direct Submission
JOURNAL      Submitted (18-DEC-2001) Genome Sequencing Center, Washington
              University School of Medicine, 4444 Forest Park Parkway, St. Louis,
              MO 63108, USA
              4 (bases 1 to 95616)
REFERENCE
AUTHORS      Waterston, R.H.
TITLE      Direct Submission
JOURNAL      Submitted (03-FEB-2002) Genome Sequencing Center, Washington
              University School of Medicine, 4444 Forest Park Parkway, St. Louis,
              MO 63108, USA
              5 (bases 1 to 95616)
REFERENCE
AUTHORS      Waterston, R.
TITLE      Direct Submission
JOURNAL      Submitted (21-FEB-2002) Department of Genetics, Washington
              University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
              On Feb 3, 2002 this sequence version replaced gi.18308880.
COMMENT
      ----- Genome Center
      Center: Washington University Genome Sequencing Center
      Center code: WUGSC
      Web site: http://genome.wustl.edu/gsc
      Contact: saplens@watson.wustl.edu
      ----- Summary Statistics
      Center project name: H_NH0383P06

```

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:  
Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:  
The RP11-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P. Y., Zhao, B., Frengen, E., Tatenno, M., Catanesi, J. J., and de Jong, P. J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. *Genomics* 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at <http://www.chori.org> VECTOR: pBACe3.6

NEIGHBORING SEQUENCE INFORMATION:  
The clone sequenced to the left is RP11-653B19, the clone sequenced to the right is RP11-332H14. Actual start of this clone is at base position 1 of RP11-383P6.



AUTHORS	DOE Joint Genome Institute and Stanford Human Genome Center.
TITLE	Direct Submission
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 132120)
AUTHORS	DOE Joint Genome Institute.
TITLE	Direct Submission
JOURNAL	Submitted (23-MAR-2000) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
REFERENCE	3 (bases 1 to 132120)
AUTHORS	DOE Joint Genome Institute and Stanford Human Genome Center.
TITLE	Direct Submission
JOURNAL	Submitted (25-JAN-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
REFERENCE	4 (bases 1 to 132120)
AUTHORS	DOE Joint Genome Institute and Stanford Human Genome Center.
TITLE	Direct Submission
JOURNAL	Submitted (15-AUG-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
COMMENT	On Aug 15, 2001 this sequence version replaced gi:12484318. Draft Sequence Produced by DOE Joint Genome Institute <a href="http://www.jgi.doe.gov">www.jgi.doe.gov</a> <a href="http://www.shgc.stanford.edu">www.shgc.stanford.edu</a> Finishing Completed at Stanford Human Genome Center Quality: Phrap Quality >=40 99.7% of Sequence; Estimated Total Number of Errors is 0.3. STS Content: SHGC-100366 G55282.
FEATURES	Location/Qualifiers
SOURCE	1..132120
	/organism="Homo sapiens"
	/mol_type="genomic DNA"
	/db_xref="taxon:9606"
	/chromosome="5"
	/clone="CTD-2325018"
BASE COUNT	44824 a 23298 c 23264 g 40734 t
ORIGIN	
Query Match	31.1%; Score 32; DB 9; Length 132120;
Best Local Similarity	58.3%; Pred. No. 50;
Matches	56; Conservative 0; Mismatches 40; Indels 0; Gaps 0;
OY	2 AAGGACGCGGAATTAACACTTTAATGACAGCATTAATAGCTCGTATNGTAGATTGGCA 61
DB	104624 AAATGGATTGGCTTCACATTTAAATTAACAAGGTATTAAGCCCATTAATAGTTCTTACAA 104565
OY	62 ATACAGTTAAAAAACGGSTATTTCCTCGTGTTCTGAT 97
DB	104564 CAGAAGCTCTATTAATGCTTTTCCATCTTACTGAT 104529
RESULT 37	
AC015774/c	157331 bp DNA linear HTG 04-SRP-2000
LOCUS	Homo sapiens clone RP11-2621, WORKING DRAFT SEQUENCE, 14 unordered pieces.
DEFINITION	AC015774
ACCESSION	AC015774
VERSION	AC015774..4 GI:9966255
KEYWORDS	HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 157331)
AUTHORS	Biren,B., Linton,L., Nusbaum,C. and Lander,E.
TITLE	Homo sapiens, clone RP11-2621
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 157331)
AUTHORS	Biren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M., Baldwin,A., Barna,N., Beckerly,R., Boguslavsky,I., Bookgalter,B., Brown,A., Castle,A., Colangelo,M., Collins,S., Collymore,A., Cooke,P., Dearellano,K., Dewar,K., Domino,M., Donelan,J., Doyle,M., Ferreira,P., FitzHugh,W., Forrest,C., Funke,R., Gage,D., Galagan,J., Gardyua,S., Grant,G., Hagos,B., Heaford,A., Horton,L.,

```

TITLE
JOURNAL
COMMENT
Center: Whitehead Institute/ MIT Center for Genome Research
Web site: http://www.seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Project Information
Center project name: IJ523
Center clone name: 2.G.21
----- Summary Statistics -----
Sequencing vector: M13; M7815; 97% of reads
Sequencing vector: Plasmid; n/a; %0.f% of reads
3.1080829015544Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 150368 bases at least Q40
Consensus quality: 153615 bases at least Q30
Consensus quality: 154711 bases at least Q20
Insert size: 163000; agarose-fp
Insert size: 156031; sum-of-contigs
Quality coverage: 4.7 in Q20 bases; agarose-fp
Quality covre:
NOTE: This is a 'working draft' sequence. It currently consists of 14 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
1
10149: contig of 10149 bp in length
10150 10249: gap of 100 bp
10250 11394: contig of 1145 bp in length
11395 11494: gap of 100 bp
11495 14270: contig of 2776 bp in length
14271 14370: gap of 100 bp
14371 19564: contig of 5194 bp in length
19565 19664: gap of 100 bp
19665 24220: contig of 4556 bp in length
24221 24320: gap of 100 bp
24321 27939: contig of 3619 bp in length
27940 28039: gap of 100 bp
28040 34728: contig of 6689 bp in length
34729 34828: gap of 100 bp
34829 42086: contig of 7258 bp in length
42087 42186: gap of 100 bp
42187 50072: contig of 7886 bp in length
50073 50172: gap of 100 bp
50173 60793: contig of 10621 bp in length
60794 60893: gap of 100 bp
60894 75258: contig of 14365 bp in length
75259 75358: gap of 100 bp
75359 92799: contig of 17441 bp in length
92800 92899: gap of 100 bp
92900 120162: contig of 27263 bp in length
120163 120262: gap of 100 bp
120263 157331: contig of 37069 bp in length.
Location/Qualifiers
1 .157331
FEATURES
SOURCE
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="RP11-2621"
/clone_lib="RPC1-11 Human Male BAC"
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  /note="assembly_fragment"
  clone_end:SP6
  vector_side:left"
misc_feature
  /note="assembly_fragment"
  10250..11394
misc_feature
  /note="assembly_fragment"
  11495..14270
misc_feature
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  24321..27939
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  /note="assembly_fragment"
  34829..42086
misc_feature
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  50173..60793
misc_feature
  /note="assembly_fragment"
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  92900..120162
misc_feature
  /note="assembly_fragment"
  120263..157331
misc_feature
  /note="assembly_fragment"
  157332..27082
BASE COUNT 51730 a 27082 c 27663 g 49552 t 1304 others
ORIGIN
Query Match 31.1%; Score 32; DB 2; Length 157331;
Best Local Similarity 58.3%; Pred. No. 49;
Matches 56; Conservative 0; Mismatches 40; Indels 0; Gaps 0;
QY 2 AAGTACGTGAGATACAGTTTATGACGATTAATAGCTCCTGCATATGCAATGCTCA 61
DB 153428 AATGTGATTGCTTCATTAATATCAAGGATTAAGCCCATTAATGTTCTTACAA 153369
QY 62 ATACAGTTAAAAACGATTTCCCTGCTTCTGAT 97
DB 153368 CAGAAGCTCTATTATGTTTCCATCTTACTGAT 153333
RESULT 38
AC103561 172387 bp DNA linear HTG 29-NOV-2001
LOCUS AC103561
DEFINITION Homo sapiens chromosome UNK clone RP11-381012, *** SEQUENCING IN
PROGRESS ***, 29 unordered pieces.
ACCESSION AC103561
VERSION AC103561.1 GI:17136164
KEYWORDS HTG; HTGS; PHASE1.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 172387)
AUTHORS Waterston,R.H.
TITLE The sequence of Homo sapiens clone
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 172387)
AUTHORS Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (28-NOV-2001) Genome Sequencing Center, Washington
UNIVERSITY School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
```

## COMMENT

```
----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
----- Project Information -----
Center project name: H_NH0381012
----- Summary Statistics -----
Sequencing vector: M13; 0%
Sequencing vector: plasmid; 100%
Chemistry: Dye-primer ET; 0% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 159141 bases at least Q40
Consensus quality: 162137 bases at least Q30
Consensus quality: 164330 bases at least Q20
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 29 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
1 1445: contig of 1445 bp in length
* 1446 1545: gap of unknown length
* 1546 3325: contig of 1680 bp in length
* 3326 3325: gap of unknown length
* 3326 4999: contig of 1674 bp in length
* 5000 5099: gap of unknown length
* 5100 6668: contig of 1569 bp in length
* 6669 6768: gap of unknown length
* 6769 9126: contig of 2358 bp in length
* 9127 9226: gap of unknown length
* 9227 11622: contig of 2396 bp in length
* 11623 11722: gap of unknown length
* 11723 14397: contig of 2675 bp in length
* 14398 14497: gap of unknown length
* 14498 17393: contig of 2896 bp in length
* 17394 17493: gap of unknown length
* 17494 19681: contig of 2188 bp in length
* 19682 19781: gap of unknown length
* 19782 21624: contig of 1843 bp in length
* 21625 21724: gap of unknown length
* 21725 24150: contig of 2426 bp in length
* 24151 24250: gap of unknown length
* 24251 26778: contig of 2528 bp in length
* 26779 26878: gap of unknown length
* 26879 29564: gap of 2686 bp in length
* 29565 29664: gap of unknown length
* 29665 34209: contig of 4545 bp in length
* 34210 34309: gap of unknown length
* 34310 36982: contig of 2673 bp in length
* 36983 37082: gap of unknown length
* 37083 41009: contig of 3927 bp in length
* 41010 41109: gap of unknown length
* 41110 44807: contig of 3698 bp in length
* 44808 44907: gap of unknown length
* 44908 49781: contig of 4874 bp in length
* 49782 49881: gap of unknown length
* 49882 56837: contig of 6956 bp in length
* 56838 63920: gap of unknown length
* 63920 64020: contig of 6983 bp in length
* 64021 72339: gap of unknown length
* 72340 72439: gap of 8319 bp in length
* 72440 79950: contig of 7511 bp in length
* 79951 80050: gap of unknown length
* 80051 87496: contig of 7446 bp in length
* 87497 87596: gap of unknown length
* 87597 102735: contig of 15139 bp in length
* 102736 102835: gap of unknown length
```

FEATURES

102836 121758: contig of 18923 bp in length

\* 121759 121858: gap of unknown length

\* 121859 141659: contig of 19801 bp in length

\* 141660 141759: gap of unknown length

\* 141760 169695: contig of 27936 bp in length

\* 169696 169795: gap of unknown length

\* 169796 170924: contig of 1129 bp in length

\* 170925 171024: gap of unknown length

\* 171025 172387: contig of 1363 bp in length.

Location/Qualifiers

1. 172387

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/mol\_type="genomic DNA"

/db\_xref="taxon:9606"

/chromosome="UNK"

/clone="RP11-381012"

1. 1445

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1546. 3325

/note="assembly\_name:Contig11"

3326. 4999

/note="assembly\_name:Contig12"

5100. 6668

/note="assembly\_name:Contig13"

6769. 9126

/note="assembly\_name:Contig14"

9227. 11622

/note="assembly\_name:Contig15"

11723. 14397

/note="assembly\_name:Contig16"

14498. 17393

/note="assembly\_name:Contig17"

17494. 19681

/note="assembly\_name:Contig18"

clone\_end:T7

vector\_side:left"

19782. 21624

/note="assembly\_name:Contig19"

21725. 24150

/note="assembly\_name:Contig20"

24251. 26778

/note="assembly\_name:Contig21"

26879. 29564

/note="assembly\_name:Contig22"

29665. 34209

/note="assembly\_name:Contig23"

34310. 36982

/note="assembly\_name:Contig24"

37083. 41009

/note="assembly\_name:Contig25"

41110. 44807

/note="assembly\_name:Contig26"

44908. 49781

/note="assembly\_name:Contig27"

49882. 56837

/note="assembly\_name:Contig28"

56938. 63920

/note="assembly\_name:Contig29"

64021. 72339

/note="assembly\_name:Contig30"

72440. 79950

/note="assembly\_name:Contig31"

80051. 87496

/note="assembly\_name:Contig32"

87597. 102735

/note="assembly\_name:Contig33"

102836. 121758

/note="assembly\_name:Contig34"

121859. 141659

/note="assembly\_name:Contig35"

141760. 169695

/note="assembly\_name:Contig36"

169796. 170924

misc\_feature /note="assembly\_name:Contig16"

171025. 172387

BASE COUNT 47364 a 37184 c 36658 g 48375 t 2806 others

ORIGIN

Query Match 31.1% Score 32; DB 2; Length 172387;

Best Local Similarity 62.5% Pred. No. 48;

Matches 50; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 17 CAGTTAATGACAGCATTAATAGCTCCTCATATGTAATGCTAATACAGTTAAATAA 76

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 20772 CAGTTGATGATTAAGAGTAAGTAATGCGTGGAGATGTGTGTAATGATTGACTCAACAATTAAC 20831

QY 77 CGGTATTTCCCTGGTCTGA 96

||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 20832 AAGTTGTGTCATGCGCTTAA 20851

RESULT 39

AC062005/c 191682 bp DNA linear HTG 20-OCT-2001

LOCUS Homo sapiens chromosome 2 clone RP11-61701 map 2, WORKING DRAFT

DEFINITION SEQUNCE. 14 unordered pieces.

AC062005

VERSION AC062005.3 GI:16303514

KEYWORDS HTG: HTGS\_PHASE1; HTGS\_DRAFT.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 191682)

ATTORNS Birren,B., Linton,L., Nusbaum,C. and Lander,E.

TITLE Homo sapiens chromosome 2, clone RP11-61701

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 191682)

ATTORNS Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,

Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F.,

Boguslavsky,L., Bouckhalter,B., Brown,A., Burkett,G.,

Campoliano,A., Castile,A., Choepel,Y., Colangelo,M., Collins,S.,

Collymore,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,D.S.,

Dodgson,S., Domingo,M., Doyle,M., Ferreira,P., Fitzhugh,W., Gage,D.,

Galagan,J., Gardyna,S., Glend,S., Goyette,M., Graham,L.,

Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L.,

Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A.,

Klein,J., Laroque,K., Lamazares,R., Landers,T., Lehotzky,J.,

Levine,R., Lieu,C., Liu,G., Locke,K., Macdonald,P., Margulis,N.,

McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPheters,R.,

Meldrum,J., Menues,L., Mihov,T., Miranda,C., Mienga,V., Morrow,J.,

Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,

O'Neill,D., Oliver,T.M., Oliver,T., Peterson,K., Pierre,N.,

Pisani,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D.,

Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B.,

Strange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,

Tessier,S., Theodore,J., Tirrell,A., Travers,M., Triggillo,J.,

Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,N.J.,

Young,G., Zainoun,J., Zimmer,A. and Zody,W.

Direct Submission

TITLE Submitted (21-APR-2000) Whitehead Institute/MIT Center for Genome

JOURNAL Research, 320 Charles Street, Cambridge, MA 02141, USA

COMMENT On Oct 20, 2001 this sequence version replaced gi:10835354.

All repeats were identified using RepeatMasker:

Smilt, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WtBR

Web site: http://www-seq.wi.mit.edu

Contact: sequence\_submissions@genome.wi.mit.edu

----- Project Information

Center Project name: L9933

Center Clone name: 617.O.1

----- Summary Statistics

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misc_feature          51637..85731
                        /note="assembly_fragment"
misc_feature          85832..103757
                        /note="assembly_fragment"
misc_feature         103858..125710
                        /note="assembly_fragment"
misc_feature         125811..147528
                        /note="assembly_fragment"
misc_feature         147629..173985
                        /note="assembly_fragment"
misc_feature         174086..191682
                        /note="assembly_fragment"
                        clone_end:T7
                        vector_side:right"
BASE COUNT          57363 a 37778 c 38363 g 56876 t 1302 others
ORIGIN
Query Match          31.1%; Score 32; DB 2; Length 191682;
Best Local Similarity 62.5%; Pred. No. 48;
Matches 50; Conservative 0; Mismatches 30; Indels 0; Gaps 0;
QY 17 CAGTTTAATGACAGCATTTATGATGCCCGCATATGTGAATTTGCTAATACAGTTAAAAA 76
Db 106077 CAGTTTAATGAAGAAGTAGTAATGCGTGAGAGATGTGTGTATGATTGATGCAACAATATTAAC 106018
QY 77 CGGTATTTCCCTGGTTCTGA 96
Db 106017 AAGTTTGTCATGCGCCCTAA 105998

RESULT 40
BX469936/c          214165 bp      DNA      linear      HTG 02-MAY-2003
LOCUS
DEFINITION
unordered pieces.
ACCESSION          BX469936
VERSION            BX469936.2 GI:30348675
KEYWORDS            HTG; HTGS_PHASE1.
SOURCE              Danio rerio (zebrafish)
ORGANISM            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                    Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
                    Cypriniformes; Cyprinidae; Danio.
                    1 (bases 1 to 214165)
                    Sims,S.
                    Direct Submission
                    Submitted (01-MAY-2003) Wellcome Trust Sanger Institute, Hinxton,
                    Cambridgeshire, CB10 1SN, UK. E-mail enquiries:
                    zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
                    On May 2, 2003 this sequence version replaced gi:30142560.
                    ----- Genome Center
                    Center: Wellcome Trust Sanger Institute
                    Center code: SC
                    Web site: http://www.sanger.ac.uk
                    Contact: zfish-help@sanger.ac.uk
                    ----- Project Information
                    Center project name: ZK32112
                    ----- Summary Statistics
                    Assembly program: XGAP4; version 4.5
                    Chemistry: Dye-terminator; 100% of reads
                    Consensus quality: 204770 bases at least Q40
                    Consensus quality: 206994 bases at least Q30
                    Consensus quality: 208843 bases at least Q20
                    Insert size: 212065; sum-of-contigs
                    Insert size: 210479; 9.8% error; agarose-fp
                    Quality coverage: 4.5% in Q20 bases; sum-of-contigs Quality
                    coverage: 4.81x in Q20 bases; agarose-fp
                    -----
                    * NOTE: This is a 'working draft' sequence. It currently
                    * consists of 22 contigs. The true order of the pieces
                    * is not known and their order in this sequence record is
                    * arbitrary. Gaps between the contigs are represented as
                    * runs of N, but the exact sizes of the gaps are unknown.

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```

URES
source
    location/Qualifiers
    1. 214165
        /organism="Danio rerio"
        /mol_type="genomic DNA"
        /db_xref="taxon:7955"
        /clone="DRKEY-32112"
        /clone_id="daniokey"
    1...3151
        /note="assembly-fragment:01542
        fragment_chain:1"
        3252..17528
        /note="assembly-fragment:01700
        fragment_chain:1"
        17629..22436
        /note="assembly-fragment:01569
        fragment_chain:1"
        22537..29373
        /note="assembly-fragment:01410
        fragment_chain:1"
        29474..51943
        /note="assembly-fragment:01600
        fragment_chain:1"
        52044..56035
        /note="assembly-fragment:00560
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        56136..80706
        /note="assembly-fragment:01101

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Query Match		30.9%	Score 31.8:	DB 2:	Length 214165;
Best Local Similarity		57.6%;	Pred. No. 53;		
Matches	57:	Conservative	0;	Mismatches	42; Indels 0; Gaps 0;
Oy	5	TGACTGGAAATACAGTTTAATGACAGCATATTATAGTCCTCATATGGAATTGCTATATA	64		
Dd	87811	TCACATGTCTTAAAGCATTGTGATAAAAGCTAAAAAAGAACAATCCAGTTCAAAATTACTTTT	8775		
Oy	65	CAGTTAAAAAAGCGTATTTCCTCGTGTTCTGATCCAACA	103		
Dd	87751	ATGTTAAAAAATACATATTTTTCAGCGTTTTTTTTCACCA	87713		
RESULT 41					
LOCUS	AC097421/c				
DEFINITION	AC097421	248948 bp	DNA	linear	HTG 10-MAY-2003
	Rattus norvegicus clone CH230-24E11.	*** SEQUENCING IN PROGRESS			
	***, 2 unordered pieces.				
ACCESSION	AC097421				
VERSION	AC097421.6	GI:30521335			
KEYWORDS	HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.				
SOURCE	Rattus norvegicus (Norway rat)				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.				



ACCESSION	AY702602	GI:29537799
VERSION	AY702602.1	
KEYWORDS		
SOURCE		
ORGANISM	Escherichia coli	
	Escherichia coli	
	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia.	
REFERENCE	1	
ATTNTHORS	Blattner, F.R., Welch, R.A. and Burland, V.D.	
TITLE	DNA sequences of Escherichia coli CPT073	
JOURNAL	Patent: WO 02059320-A 188 01-AUG-2002;	
	WISCONSIN ALUMNI RESEARCH FOUNDATION (US)	
FEATURES	location/Qualifiers	
SOURCE	1..1604	
	/organism="Escherichia coli"	
	/mol_type="genomic DNA"	
	/db_xref="taxon:562"	
BASE COUNT	534 a 247 c 276 g 547 t	
ORIGIN		
Query Match	30.7%; Score 31.6; DB 6; Length 1604;	
Best Local Similarity	56.9%; Pred. No. 1.le+02;	
Matches	58; Conservative 0; Mismatches 44; Indels 0; Gaps 0;	
OY	2 AAGGACATGGAATACAGTTTAATGACAGCATTAATAGCTCTCATATGTAATTCCTA 61	
Db	1130 AAGGAATGATGATGATATTTTATTTATTTGCGAAGATGAAAGATCTGCAAAATGTTTCCTT 1071	
OY	62 ATACAGTTAAAAAAGCGTAATTCCTGCTGTTCTGATCCACA 103	
Db	1070 TTTGGACAATACAAAACACTCATCCAGATCTGATTTGATCA 1029	
RESULT 43		
AC112392_1/c		
WPCOMMENT		
Sequence split into 5 fragments	LOCUS AC112392 Accession AC112392	
Fragment Name	Begin	End
AC112392_0	1	110000
AC112392_1	100001	210000
AC112392_2	200001	310000
AC112392_3	300001	410000
AC112392_4	400001	479080
Continuation (2 of 5) of AC112392	from base 100001 (AC112392 Rattus norvegicus clone CH2	
Query Match	30.7%; Score 31.6; DB 2; Length 110000;	
Best Local Similarity	74.1%; Pred. No. 65;	
Matches	40; Conservative 0; Mismatches 14; Indels 0; Gaps 0;	
OY	32 ATTATAGCTCCGATATGTAATTCCTAATACAGTTAAAAAAGCGTATTTTC 85	
Db	102879 ATTACTAGAGCGCTCTTATGTGAGACTACGACAACTCTCAAGAAACAGTATTTTC 102826	
RESULT 44		
AC112392_2/c		
WPCOMMENT		
Sequence split into 5 fragments	LOCUS AC112392 Accession AC112392	
Fragment Name	Begin	End
AC112392_0	1	110000
AC112392_1	100001	210000
AC112392_2	200001	310000
AC112392_3	300001	410000
AC112392_4	400001	479080
Continuation (3 of 5) of AC112392	from base 200001 (AC112392 Rattus norvegicus clone CH2	
Query Match	30.7%; Score 31.6; DB 2; Length 110000;	
Best Local Similarity	74.1%; Pred. No. 65;	
Matches	40; Conservative 0; Mismatches 14; Indels 0; Gaps 0;	
OY	32 ATTATAGCTCCGATATGTAATTCCTAATACAGTTAAAAAAGCGTATTTTC 85	
Db	2879 ATTACTAGAGCGCTCTTATGTGAGACTACGACAACTCTCAAGAAACAGTATTTTC 2826	

RESULT 45	AC124223 0/c	MPCOMMENT
Sequence split into 5 fragments	LOCUS AC124223	Accession AC124223
Fragment Name	Begin	End
AC124223_0	1	110000
AC124223_1	100001	210000
AC124223_2	200001	310000
AC124223_3	300001	410000
AC124223_4	400001	448185
AC124223		448185 bp
DEFINITION	Rattus norvegicus clone CH230-486P3, *** SQUENCING IN PROGRESS	HTG 12-OCT-2002
ACCESSION	AC124223	
VERSION	AC124223.3 GI:23915271	
KEYWORDS	HTG: HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.	
SOURCE	Rattus norvegicus (Norway rat)	
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.	
REFERENCE	1 (bases 1 to 448185)	
AUTHORS	Muzny,D,Marle, Metzker,M, Lee, Abramzon,S, Adams,C, Alder,J, Allen,C, Allen,H, Alsbrooks,S, Amin,A, Angiano,D, Anyaldebech,Y, Aoyagi,A, Ayodeji,M, Baca,E, Baden,H, Baldwin,D, Bandaranaike,D, Barber,M, Barnstead,M, Benahmed,F, Biewalo,K, Blair,J, Blankenburg,K, Blyth,P, Brown,M, Bryant,N, Buhay,C, Burch,P, Burrell,K, Calderon,E, Cardenas,V, Carter,K, Cavazos,I, Caesar,H, Center,A, Chacko,J, Chavez,D, Chen,G, Chen,R, Chen,Y, Chen,Z, Chu,J, Cleveland,C, Cockrell,R, Cox,C, Coyle,M, Cree,A, D'Souza,L, Davila,M,L, Davis,C, Davy-Carroll,L, De Anda,C, Dederich,D, Delgado,O, Denison,S, Deramo,C, Ding,Y, Dinh,H, Divya,K, Draper,H, Dugan-Rocha,S, Dunn,A, Durbin,K, Duvall,B, Eaves,K, Egan,A, Escotto,M, Eugene,C, Evans,C,A, Falls,T, Fan,G, Fernandez,S, Finley,M, Flagg,N, Forbes,L, Foster,M, Foster,P, Fraser,C,M, Gabisi,A, Ganta,R, Garcia,A, Garner,T, Garza,M, Georgegeorgis,E, Geer,K, Gill,R, Grady,M, Guerra,M, Guevara,W, Gunaratne,P, Haaland,W, Hamli,C, Hamilton,C, Hamilton,K, Haverly,Y, Havlak,P, Hawes,A, Henderson,N, Hernandez,J, Hernandez,R, Hines,S, Hladun,S,L, Hodgson,A, Hogues,M, Hollins,B, Howells,S, Hulak,S, Hume,J, Idlebird,D, Jackson,A, Jackson,L, Jacob,L, Jiang,H, Johnson,B, Johnson,R, Jolivet,A, Karpachy,S, Kelly,S, Kelly,S, Khan,Z, King,L, Kovar,C, Kowis,C, Kraft,C,L, Lebow,H, Levan,J, Lewis,L, Li,Z, Liu,J, Liu,J, Liu,W, Liu,Y, London,P, Longacre,S, Lopez,J, Lorenshewa,L, Louissege,H, Locardo,R,J, Lu,X, Ma,J, Maheshwari,M, Mahindartne,M, Mahmoud,M, Malloy,K, Mangun,A, Mangum,B, Mapua,P, Martin,K, Martin,R, Martinez,E, Mathney,S, McLeod,P, McNeill,T,Z, Meenen,E, Milosavljevic,A, Miner,G, Minja,E, Montemayor,J, Moore,S, Morgan,M, Morris,K, Morris,S, Mundasa,M, Murphy,M, Nair,L, Nankervis,C, Neal,D, Newton,N, Nguyen,N, Norris,S, Nwakoelomoh,O, Okwono,G, Olarpungagoon,A, Pal,S, Parks,K, Pasternak,S, Paul,H, Perez,A, Perez,L, Pfannkoch,C, Plopper,F, Poindeexter,A, Popovic,D, Prins,E, Pu,L, Puzo,M, Quiroz,J, Rachlin,E, Reeves,K, Reigel,M,A, Reigh,R, Reilly,B, Reilly,M, Ren,Y, Reuter,M, Richards,S, Riggs,F, Rives,C, Rodkey,T, Rojas,A, Rose,M, Rose,R, Ruiz,S, Sanders,W, Savery,G, Scherer,S, Scott,G, Shatman,S, Shen,H, Shetty,J, Shvartsbeyan,A, Sisson,I, Sitter,C,D, Smaj,D, Sneed,A, Sodergren,E, Song,X,Z, Sorelle,R, Sosa,J, Steimle,M, Strong,R, Sutton,A, Swatek,A, Taber,P, Taylor,C, Taylor,T, Thomas,N, Thomas,S, Tingey,A, Trejos,Z, Usmani,K, Valas,R, Vera,V, Villasant,D, Waldron,L, Walker,B, Wang,J, Wang,Q, Wang,S, Warren,J, Warren,R, Wei,X, White,F, Williams,G, Willson,R, Wlecyk,R, Wooden,H, Worley,K, Wright,D, Wright,R, Wu,J, Yakub,S, Yen,J, Yoon,L, Yoon,V, Yu,F, Zhang,J, Zhou,J, Zhou,X, Zhao,S, Dunn,D, von Niederhausern,A, Weiss,R, Smith,D,R, Holt,R,A, Smith,H,O, Weinstock,G, and Gibbs,R,A.	

TITLE Direct Submission  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 448185)  
AUTHORS Worley, K.C.  
JOURNAL Direct Submission  
Submitted (14-JUN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
3 (bases 1 to 448185)  
Rat Genome Sequencing Consortium.  
Submitted (12-OCT-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
On Oct 12, 2002 this sequence version replaced gi:21465216.  
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center  
Center: Baylor College of Medicine  
Center code: BCM  
Web site: <http://www.hgsc.bcm.tmc.edu/>  
Contact: hgsc-help@bcm.tmc.edu

----- Project Information  
Center project name: KA0Z  
Center clone name: CH230-486P3

----- Summary Statistics  
Assembly program: Phrap; version 0.990329  
Consensus quality: 355484 bases at least Q40  
Consensus quality: 369229 bases at least Q30  
Estimated insert size: 496298; sum-of-contigs estimation  
Quality coverage: 5x in Q20 bases; sum-of-contigs estimation

\* NOTE: Estimated insert size may differ from sequence length  
(see [http://www.hgsc.bcm.tmc.edu/docs/genbank\\_craft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/genbank_craft_data.html))  
\* NOTE: This sequence may represent more than one clone.  
\* NOTE: This is a 'working draft' sequence. It currently consists of 25 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

1 26070: contig of 26070 bp in length  
\* 26071 26170: gap of unknown length  
\* 26171 83555: contig of 57485 bp in length  
\* 83556 83755: gap of unknown length  
\* 83756 98687: contig of 14932 bp in length  
\* 98688 98787: gap of unknown length  
\* 98788 119532: contig of 20745 bp in length  
\* 119533 119632: gap of unknown length  
\* 119633 130323: contig of 10691 bp in length  
\* 130324 130423: gap of unknown length  
\* 130424 158608: contig of 28185 bp in length  
\* 158609 158708: gap of unknown length  
\* 158709 169812: contig of 11104 bp in length  
\* 169813 169912: gap of unknown length  
\* 169913 201720: contig of 31808 bp in length  
\* 201721 201820: gap of unknown length  
\* 201821 217149: contig of 15329 bp in length  
\* 217150 217249: gap of unknown length  
\* 217250 244384: contig of 27135 bp in length

244385 244484: gap of unknown length  
\* 244485 248149: contig of 3665 bp in length  
\* 248150 248249: gap of unknown length  
\* 248250 253526: contig of 5277 bp in length  
\* 253527 253626: gap of unknown length  
\* 253627 266141: contig of 12514 bp in length  
\* 266141 266240: gap of unknown length  
\* 266241 284166: contig of 17926 bp in length  
\* 284167 284266: gap of unknown length  
\* 284267 288035: contig of 3769 bp in length  
\* 288036 288135: gap of unknown length  
\* 288136 351975: contig of 63840 bp in length  
\* 351976 352075: gap of unknown length  
\* 352076 356720: contig of 4645 bp in length  
\* 356721 356820: gap of unknown length  
\* 356821 367631: contig of 10811 bp in length  
\* 367632 367731: gap of unknown length  
\* 367732 388952: contig of 21221 bp in length  
\* 388953 390382: gap of unknown length  
\* 390383 390482: gap of unknown length  
\* 390483 394515: contig of 4033 bp in length  
\* 394516 394615: gap of unknown length  
\* 394616 400601: contig of 5966 bp in length  
\* 400602 400701: gap of unknown length  
\* 400702 410562: contig of 9861 bp in length  
\* 410563 410662: gap of unknown length  
\* 410663 416153: contig of 5491 bp in length  
\* 416154 416253: gap of unknown length  
\* 416254 448185: contig of 31932 bp in length.

## FEATURES

## source

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/organism="Rattus norvegicus"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:10116"  
/clone="CH230-486P3"

## misc\_feature

1..4191  
/note="wgs\_end\_extension  
clone\_end:Sp6"  
6779..7355  
/note="wgs\_clone boundary  
clone\_end:Sp6  
site:Mbol

## misc\_feature

end\_sequence:RXBQM6TY"  
14709..18698  
/note="wgs\_contig"  
19740..26070  
/note="wgs\_contig"

## misc\_feature

26171..27385  
/note="wgs\_contig"  
32433..41624  
/note="wgs\_contig"  
42273..44529  
/note="wgs\_contig"

## misc\_feature

44580..48089  
/note="wgs\_contig"  
48484..51371  
/note="wgs\_contig"

## misc\_feature

Query Match 30.7%; Score 31.6; DB 2; Length 110000;  
Best Local Similarity 74.1%; Pred. No. 65;  
Matches 40; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

OY 32 ATTATAGCCTGCATATGCAATGCTTAATACAGTTAAACGATATTTC 85  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
DB 74161 ATTACTAGAGCCTGCTTATGTGTAACCTACAGAACTCTCAAGAAAACAGTATTTC 74108

Search completed: August 25, 2003, 07:22:02  
Job time : 1605 secs

FILE REFERENCE: CL001160

Query Match	28.0%;	Score 28.8;	DB 4;	Length 1830121;
Best Local Similarity	58.0%;	Pred. NO. 9.8;		

Db 1541171 AAAATATTAATTCCTGATTTCTCATTCGA 1541144



;; PRIOR FILING DATE: 1998-06-05  
;; PRIOR APPLICATION NUMBER: 60/088217  
;; PRIOR FILING DATE: 1998-06-05  
;; PRIOR APPLICATION NUMBER: 60/088655  
;; PRIOR FILING DATE: 1998-06-09  
;; PRIOR APPLICATION NUMBER: 60/088734  
;; PRIOR FILING DATE: 1998-06-10  
;; PRIOR APPLICATION NUMBER: 60/088738  
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;; PRIOR FILING DATE: 1998-06-10  
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;; PRIOR FILING DATE: 1998-06-23  
;; PRIOR APPLICATION NUMBER: 60/090429  
;; PRIOR FILING DATE: 1998-06-24  
;; PRIOR APPLICATION NUMBER: 60/090431  
;; PRIOR FILING DATE: 1998-06-24  
;; PRIOR APPLICATION NUMBER: 60/090435  
;; PRIOR FILING DATE: 1998-06-24  
;; PRIOR APPLICATION NUMBER: 60/090444  
;; PRIOR FILING DATE: 1998-06-24

;; PRIOR APPLICATION NUMBER: 60/090445  
;; PRIOR FILING DATE: 1998-06-24  
;; PRIOR APPLICATION NUMBER: 60/090472  
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;; PRIOR APPLICATION NUMBER: 60/090535  
;; PRIOR FILING DATE: 1998-06-24  
;; PRIOR APPLICATION NUMBER: 60/090540  
;; PRIOR FILING DATE: 1998-06-24  
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;; PRIOR FILING DATE: 1998-06-25  
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;; PRIOR FILING DATE: 1998-06-26  
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;; PRIOR FILING DATE: 1998-06-26  
;; PRIOR APPLICATION NUMBER: 60/091360  
;; PRIOR FILING DATE: 1998-07-01  
;; PRIOR APPLICATION NUMBER: 60/091478  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091544  
;; PRIOR FILING DATE: 1998-07-01  
;; PRIOR APPLICATION NUMBER: 60/091519  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091626  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091633  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091978  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/091982  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/092182  
;; PRIOR FILING DATE: 1998-07-09

Query Match 27.2%; Score 28; DB 4; Length 466;  
Best Local Similarity 59.7%; Pred. No. 2.4;  
Matches 46; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

OY 5 TGACGTGATTAACAGTTTAAACAGCATTATAGCTCTGATATGTAATTCCTAATA 64  
DB 216 TGACGTGTTTAAATCTTTATGATGATTAATAACAGCTGATATGTAATTCACCA 157  
OY 65 CAGTTAAAAAAGGTA 81  
DB 156 CCCTGTAATAAATAGTA 140

RESULT 7  
US-08-981-601-26/c  
Sequence 26, Application US/08981601  
Patent No. 6133023  
GENERAL INFORMATION:  
APPLICANT: MADSEN, Soeren Michael  
APPLICANT: VRANG, Astrid  
APPLICANT: ARNAU, Jose  
APPLICANT: RAVN, Peter  
APPLICANT: GROENVOLD JOHNSSEN, Mads  
APPLICANT: ISRAEISEN, Hans  
TITLE OF INVENTION: A LACTIC ACID BACTERIAL REGULATABLE  
EXPRESSION SYSTEM



NUMBER OF SEQUENCES: 30  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FOLEY & LARDNER  
STREET: 3000 K Street, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/981,601  
FILING DATE: 29-DEC-1997  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/DK97/00341  
FILING DATE: 22-AUG-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/711,434  
FILING DATE: 06-SEP-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Bent, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 030307/0158  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 672-5300  
TELEFAX: (202) 672-5399  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 170 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-981-601-26  
Query Match 26.8%; Score 27.6; DB 3; Length 170;  
Best Local Similarity 67.2%; Pred. No. 2.6;  
Matches 39; Conservative 0; Mismatches 19; Indels 0; Caps 0;  
QY 33 TTAATGCTCTCGATATGCAATGCTATACAGTTAAACGCTATTTCCCTGG 90  
DB 116 TGAAGAATATATGTGAATTAATGCAATATAGTCAATTAATAATGCTTTTTCGG 59  
RESULT 8  
US-08-179-557-17/C  
Sequence 17, Application US/08179557  
Patent No. 5837509  
GENERAL INFORMATION:  
APPLICANT: ISRAELSEN, Hans  
APPLICANT: BECH HANSEN, Egon  
APPLICANT: MADSEN, Soeren Michael  
APPLICANT: JOHANSEN, Eric  
APPLICANT: NILSSON, Dan  
APPLICANT: VRANG, Astrid  
TITLE OF INVENTION: Recombinant Lactic Acid Bacterium  
TITLE OF INVENTION: Containing an Inserted Promoter and Method of Constructing  
TITLE OF INVENTION: Same  
NUMBER OF SEQUENCES: 39  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W.  
CITY: Washington, D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/179,557  
FILING DATE: 07-JAN-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DK 1579/92  
FILING DATE: 30-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DK 0988/93  
FILING DATE: 01-SEP-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/DK94/00004  
FILING DATE: 03-JAN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/036,681  
FILING DATE: 25-MAR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 30307/140/PLVI  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202 672 5300  
TELEFAX: 202 672 5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1070 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-179-557-17  
Query Match 26.8%; Score 27.6; DB 2; Length 1070;  
Best Local Similarity 67.2%; Pred. No. 4;  
Matches 39; Conservative 0; Mismatches 19; Indels 0; Caps 0;  
QY 33 TTAATGCTCTCGATATGCAATGCTATACAGTTAAACGCTATTTCCCTGG 90  
DB 1016 TGAAGAATATATGTGAATTAATGCAATATAGTCAATTAATAATGCTTTTTCGG 959  
RESULT 9  
US-08-200-900A-1  
Sequence 1, Application US/08200900A  
Patent No. 5665566  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: CLONING OF ENTEROKINASE AND METHOD OF USE  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genetics Institute, Inc. - Legal Affairs  
STREET: 87 CambridgePark Drive  
CITY: Cambridge  
STATE: MA  
COUNTRY: USA  
ZIP: 02140  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/200,900A  
FILING DATE: 23-FEB-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Meiner, Maureen C.  
REGISTRATION NUMBER: 31,544  
REFERENCE/DOCKET NUMBER: GI 5201-FWC  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 876-1170 X8574  
TELEFAX: (617) 876-5851

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; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 2581 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: cDNA
US-08-200-900A-1

Query Match
Best Local Similarity 55.1%; Score 27.6; DB 1; Length 2581;
Matches 54; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 3 ACTGACTGGAATTAACAGTTTAATGACAGCATTAATAGCTTCGATATGTGAATTGCTAA 62
DB 2469 AGTTAAAAAAATAATTAATTAATAAAGTCTGATCTTACCTAAGGCACTGAATGCTAC 2528
QY 63 TACAGTTAAAAAAGCGTAATTCCTCGTTCTGATCCA 100
DB 2529 AAAAAAAGGCGAATTCAGCTTGACCTTAACCA 2566

RESULT 10
PCT-US94-00616-1
; Sequence 1, Application PC/TUS9400616
; GENERAL INFORMATION:
;   APPLICANT:
;   TITLE OF INVENTION: CLONING OF ENTEROKINASE AND METHOD OF USE
;   NUMBER OF SEQUENCES: 33
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   OPERATING SYSTEM: IBM PC compatible
;   SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: PCT/US94/00616
;   FILING DATE:
;   CLASSIFICATION:
;   INFORMATION FOR SEQ ID NO: 1:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 2581 base pairs
;     TYPE: nucleic acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
;     MOLECULE TYPE: cDNA
PCT-US94-00616-1

Query Match
Best Local Similarity 55.1%; Score 27.6; DB 5; Length 2581;
Matches 54; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 3 AGTACTGGAATTAACAGTTTAATGACAGCATTAATAGCTTCGATATGTGAATTGCTAA 62
DB 2469 AGTTAAAAAAATAATTAATTAATAAAGTCTGATCTTACCTAAGGCACTGAATGCTAC 2528
QY 63 TACAGTTAAAAAAGCGTAATTCCTCGTTCTGATCCA 100
DB 2529 AAAAAAAGGCGAATTCAGCTTGACCTTAACCA 2566

RESULT 11
US-09-484-970B-138
; Sequence 138, Application US/09484970B
; Patent No. 6426186
; GENERAL INFORMATION:
;   APPLICANT: Jones, Karen A.
;   APPLICANT: Volkmut, Wayne
;   APPLICANT: Walker, Michael G.
;   TITLE OF INVENTION: BONE REMODELING GENES
;   FILE REFERENCE: PB-0014 US
;   CURRENT APPLICATION NUMBER: US/09/484, 970B
;   CURRENT FILING DATE: 2000-01-18
;   NUMBER OF SEQ ID NOS: 172
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; SOFTWARE: PERL Program
; SEQ ID NO 138
; LENGTH: 3054
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID NO. 6426186 336987.1CBI
US-09-484-970B-138

Query Match
Best Local Similarity 56.7%; Score 27.6; DB 4; Length 3054;
Matches 51; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

QY 13 ATACAGTTTAATGACAGCATTAATAGCTTCGATATGTGAATTGCTAATACGTTAA 72
DB 2256 ATAGAGAGCTTACTATATATATATATATTAATAGTGCATATATTTACTTCAATACCTATATT 2315
QY 73 AAAACGTAATTCCTCGTTCTGATCCAAC 102
DB 2316 AGAAGATATGTGCTGACTGAATATATAC 2345

RESULT 12
US-09-539-333D-196
; Sequence 196, Application US/09539333D
; Patent No. 6476208
; GENERAL INFORMATION:
;   APPLICANT: Cohen, Daniel
;   APPLICANT: Blumenfeld, Marta
;   APPLICANT: Chumakov, Ilya
;   APPLICANT: Bougueleret, Lydie
;   APPLICANT: Bihain, Bernard
;   APPLICANT: Essiloux, Laurent
;   TITLE OF INVENTION: SCHIZOPHRENIA ASSOCIATED GENES, PROTEINS AND BIALLELIC MARKERS
;   FILE REFERENCE: GENSET 047AUS
;   CURRENT APPLICATION NUMBER: US/09/539, 333D
;   CURRENT FILING DATE: 2000-03-30
;   PRIOR APPLICATION NUMBER: US 60/126,903
;   PRIOR FILING DATE: 1999-03-30
;   PRIOR APPLICATION NUMBER: US 60/131,971
;   PRIOR FILING DATE: 1999-04-30
;   PRIOR APPLICATION NUMBER: US 60/132,065
;   PRIOR FILING DATE: 1999-04-30
;   PRIOR APPLICATION NUMBER: US 60/143,928
;   PRIOR FILING DATE: 1999-07-14
;   PRIOR APPLICATION NUMBER: US 60/145,915
;   PRIOR FILING DATE: 1999-07-27
;   PRIOR APPLICATION NUMBER: US 60/146,453
;   PRIOR FILING DATE: 1999-07-29
;   PRIOR APPLICATION NUMBER: US 60/146,452
;   PRIOR FILING DATE: 1999-07-29
;   PRIOR APPLICATION NUMBER: US 60/162,288
;   PRIOR FILING DATE: 1999-10-28
;   PRIOR APPLICATION NUMBER: US 09/416,384
;   PRIOR FILING DATE: 1999-10-12
;   NUMBER OF SEQ ID NOS: 231
;   SOFTWARE: Patent.pm
;   SEQ ID NO 196
;   LENGTH: 3001
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
;   FEATURE:
;     NAME/KEY: allele
;     LOCATION: 1501
;   OTHER INFORMATION: 99-26228-172 : polymorphic base G or C
;   NAME/KEY: misc_binding
;     LOCATION: 1482..1500
;   OTHER INFORMATION: 99-26228-172.m1s1
;   NAME/KEY: misc_binding
;     LOCATION: 1502..1521
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; OTHER INFORMATION: 99-26228-172.ms2, complement
; FEATURE:
; NAME/KEY: primer.blind
; LOCATION: 1330..1350
; OTHER INFORMATION: upstream amplification primer
; FEATURE:
; NAME/KEY: primer.blind
; LOCATION: 1792..1812
; OTHER INFORMATION: downstream amplification primer, complement
; FEATURE:
; NAME/KEY: misc.binding
; LOCATION: 1489..1513
; OTHER INFORMATION: 99-26228-172 probe
US-09-539-333D-196

Query Match      26.6%; Score 27.4; DB 4; Length 3001;
Best Local Similarity 55.9%; Pred. No. 6;
Matches 52; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

QY 3 AGTGAAGTGAATAAGAGTTAATGACAGCATTTAGCTTCCTGATATGGAATGCTAA 62
Db 418 AATGACATGACGAGGACATTTAGCTGCAATAATATAGAGTTATAGTAATGTGATAT 477
QY 63 TACAGTTAAAAAAGCGTATTTCCCTGTTCTG 95
Db 478 CCAGGTAATAAAGACGTATTTTCCCAATCTG 510

RESULT 13
US-09-220-132-2
; Sequence 2, Application US/09220132
; Patent No. 6506607
; GENERAL INFORMATION:
; APPLICANT: Shyjan, Andrew W.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE IDENTIFICATION AND ASSESSMENT
; FILE REFERENCE: 07334-074001
; CURRENT APPLICATION NUMBER: US/09/220,132
; CURRENT FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: US 60/079,303
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: US 60/068,821
; PRIOR FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 191
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 5508
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-220-132-2

Query Match      26.6%; Score 27.4; DB 4; Length 5508;
Best Local Similarity 62.3%; Pred. No. 6;
Matches 43; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 26 GACAGCATTAATAGCTTCCTGATATGGAATGCTTAATAGTTAAAAAAGGATATTC 85
Db 557 GACAGCTGAAAAAGCATATGACAACTGAATCTAAATATAGGAAAAAGTCCCTATTAA 616
QY 86 CCGTGTCT 94
Db 617 TTGTGTTGT 625

RESULT 14
US-09-410-464-9
; Sequence 9, Application US/09410464
; Patent No. 6395892
; GENERAL INFORMATION:
; APPLICANT: Strauss et al.
; TITLE OF INVENTION: Floral homeotic genes for manipulation of flowering in
; FILE REFERENCE: 53375
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; CURRENT APPLICATION NUMBER: US/09/410,464
; CURRENT FILING DATE: 1999-10-01
; EARLIER APPLICATION NUMBER: 09/287,700
; EARLIER FILING DATE: 1999-04-06
; EARLIER APPLICATION NUMBER: 60/080,851
; EARLIER FILING DATE: 1998-04-06
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 11485
; TYPE: DNA
; ORGANISM: Populus balsamifera subsp. trichocarpa
US-09-410-464-9

Query Match      26.6%; Score 27.4; DB 4; Length 11485;
Best Local Similarity 57.6%; Pred. No. 8.3;
Matches 49; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY 13 ATAAAGCTTAATGACAGCATTAATAGCTCCTGATATGGAATGCTTAATAGCTTAA 72
Db 6634 ATAAAGCAATTAATAAATTAATTAATTTATTTTATTAATTAATAAATTAATA 6693
QY 73 AAAACGCTATTTCCCTGTTCTGAT 97
Db 6694 AACACAGTATTACCAATATACAGAT 6718

RESULT 15
US-09-734-674-3/C
; Sequence 3, Application US/09734674
; Patent No. 6498022
; GENERAL INFORMATION:
; APPLICANT: Wei, Ming-Hui et al.
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
; FILE REFERENCE: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
; FILE REFERENCE: CLO01018
; CURRENT APPLICATION NUMBER: US/09/734,674
; CURRENT FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 202001
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(202001)
; OTHER INFORMATION: n = A,T,C or G
US-09-734-674-3

Query Match      26.6%; Score 27.4; DB 4; Length 202001;
Best Local Similarity 62.3%; Pred. No. 17;
Matches 43; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 5 TGACTGAATTAACGTTAATGACAGCATTAATAGCTTCCTGATATGGAATGCTTATA 64
Db 93512 TCATAGCAATTAATCTTGTGAGAAAGCATTAAGAAATTAATTAAGAAAGTGAAGA 93453
QY 65 CAGTTAAA 73
Db 93452 CTGGTAAA 93444

RESULT 16
US-09-328-352-1715/C
; Sequence 1715, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACT
; FILE REFERENCE: GTC99-038A
```



```

RESULT 21
US-09-791-211-10/c
? Sequence 10, Application US/09791211
? Patent No. 6448080
? GENERAL INFORMATION:
? APPLICANT: Donna T. Ward
? APPLICANT: Andrew T. Watt
? TITLE OR INVENTION: ANTISENSE MODULATION OF WRN EXPRESSION
? FILE REFERENCE: RTS-0205
? CURRENT APPLICATION NUMBER: US/09/791,211
? CURRENT FILING DATE: 2001-02-23
? NUMBER OF SEQ ID NOS: 90
? SEQ ID NO 10
? LENGTH: 98844
? TYPE: DNA
? ORGANISM: Homo sapiens
? FEATURE:
? NAME/KEY: unsure
? LOCATION: 24962
? OTHER INFORMATION: unknown
? NAME/KEY: unsure
? LOCATION: 64383
? OTHER INFORMATION: unknown
? NAME/KEY: unsure
? LOCATION: 65468
? OTHER INFORMATION: unknown
? NAME/KEY: unsure
? LOCATION: 65469
? OTHER INFORMATION: unknown

```

40; conical valve 0; maxilla closed



```
COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/092,409
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/680,736
; FILING DATE: 12-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Connell, Gary J.
; REGISTRATION NUMBER: 32,020
; REFERENCE/DOCKET NUMBER: 2618-46-C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 863-9700
; TELEFAX: (303) 863-0223
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1038 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1035
; US-09-092-409-53
```

```
Query Match      25.8%; Score 26.6; DB 3; Length 1038;
Best Local Similarity 60.3%; Pred. No. 8.4;
Matches 44; Conservative 0; Mismatches 29; Indels 0; Gaps 0;
```

```
QY      13 ATAAAGTTTAATGACGATTATAGCTCTGCATATGCAATTGCTAATACAGTTAA 72
        ||| ||| | | | | | | | | | | | | | | | | | | | | | | |
DB      640 AAAAAGTTCATGCTCACTTTGATGCTCTACAGATCTAGATTCTTACACATTCCA 581
```

```
OY      73 AAACGGTATTTC 85
        ||| | | | |
DB      580 TAAAGTTGGTTC 568
```

```
RESULT 26
US-08-220-151-18/C
; Sequence 18, Application US/08220151
; Patent No. 5529780
; GENERAL INFORMATION:
; APPLICANT: Paoletti, Enzo
; TITLE OF INVENTION: NUCLEOTIDE AND AMINO ACID SEQUENCES OF
; TITLE OF INVENTION: CANINE HERPESVIRUS gB, gC AND gD AND USES THEREFOR
; NUMBER OF SEQUENCES: 91
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris & Safford
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/220,151
; FILING DATE: 30-MAR-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Frommer, William S.
; REGISTRATION NUMBER: 25,506
```

```
REFERENCE/DOCKET NUMBER: 454310-2540
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 840-3333
; TELEFAX: (212) 840-0712
; TELEX: 425066 CURTMS
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1320 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-220-151-18
```

```
Query Match      25.8%; Score 26.6; DB 1; Length 1320;
Best Local Similarity 60.3%; Pred. No. 8.9;
Matches 44; Conservative 0; Mismatches 29; Indels 0; Gaps 0;
```

```
QY      13 ATAAAGTTTAATGACGATTATAGCTCTGCATATGCAATTGCTAATACAGTTAA 72
        ||| ||| | | | | | | | | | | | | | | | | | | | | | |
DB      840 AAAAAGTTCATGCTCACTTTGATGCTCTACAGATCTAGATTCTTACACATTCCA 781
```

```
OY      73 AAACGGTATTTC 85
        ||| | | | |
DB      780 TAAAGTTGGTTC 768
```

```
RESULT 27
US-08-413-118-18/C
; Sequence 18, Application US/08413118
; Patent No. 5688920
; GENERAL INFORMATION:
; APPLICANT: PAOLETTI, ENZO
; TITLE OF INVENTION: NUCLEOTIDE AND AMINO ACID SEQUENCES OF
; TITLE OF INVENTION: CANINE HERPESVIRUS gB, gC, AND gD AND USES THEREFOR
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CURTIS, MORRIS & SAFFORD, P.C.
; STREET: 530 FIFTH AVENUE, 25TH FLOOR
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/413,118
; FILING DATE: 29-MAR-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/220,151
; FILING DATE: 30-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: FROMMER, WILLIAM S.
; REGISTRATION NUMBER: 25,506
; REFERENCE/DOCKET NUMBER: 454310-2670
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 840-3333
; TELEFAX: (212) 840-0712
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1320 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-413-118-18
```

```
Query Match      25.8%; Score 26.6; DB 1; Length 1320;
```





```

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/473,446
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/413,118
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: FROMMER, WILLIAM S.
; REGISTRATION NUMBER: 25,506
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 840-3333
; TELEFAX: (212) 840-0712
; INFORMATION FOR SEQ ID NO: 126:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1415 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-473-446-126

Query Match      25.8%; Score 26.6; DB 3; Length 1415;
Best Local Similarity 60.3%; Pred. No. 9.1;
Matches 44; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY      13 ATAAAGTTTAATGACAGCATTAATAGCTCTGCATATGATGCTTCTAATACAGTTAA 72
      1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB      939 AAAAAGTTCATGCTCAACTTTGATGCTCTACAGATCTAGATCTTACACCATTC 880
      1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      73 AAACGGTATTTC 85
      1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB      879 TAAAGTTGGTTC 867

RESULT 31
US-08-680-726A-51/C
; Sequence 51, Application US/08680726A
; Patent No. 5804197
; GENERAL INFORMATION:
; APPLICANT: Haanes, Elizabeth J.
; TITLE OF INVENTION: RECOMBINANT CANINE HERPESVIRUSES
; NUMBER OF SEQUENCES: 92
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheridan Ross & McIntosh
; STREET: 1700 Lincoln Street, Suite 3500
; CITY: Denver
; STATE: Colorado
; COUNTRY: U.S.A.
; ZIP: 80203
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/680,726A
; FILING DATE: 12-JUL-1996.
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Connell, Gary J.
; REGISTRATION NUMBER: 32,020
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 863-9700
; TELEFAX: (303) 863-0223
; INFORMATION FOR SEQ ID NO: 51:
; MOLECULE TYPE: DNA (genomic)
```

```

; SEQUENCE CHARACTERISTICS:
; LENGTH: 10592 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-680-726A-51

Query Match      25.8%; Score 26.6; DB 1; Length 10592;
Best Local Similarity 60.3%; Pred. No. 15;
Matches 44; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY      13 ATAAAGTTTAATGACAGCATTAATAGCTCTGCATATGGAATTGCTAATACAGTTAA 72
      1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB      4826 AAAAAGTTCATGCTCAACTTTGATGCTCTACAGATCTAGATCTTACACCATTC 4885
      1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      73 AAACGGTATTTC 85
      1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB      4886 TAAAGTTGGTTC 4898

RESULT 32
US-08-680-726A-52
; Sequence 52, Application US/08680726A
; Patent No. 5804197
; GENERAL INFORMATION:
; APPLICANT: Haanes, Elizabeth J.
; TITLE OF INVENTION: RECOMBINANT CANINE HERPESVIRUSES
; NUMBER OF SEQUENCES: 92
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheridan Ross & McIntosh
; STREET: 1700 Lincoln Street, Suite 3500
; CITY: Denver
; STATE: Colorado
; COUNTRY: U.S.A.
; ZIP: 80203
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/680,726A
; FILING DATE: 12-JUL-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Connell, Gary J.
; REGISTRATION NUMBER: 32,020
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 863-9700
; TELEFAX: (303) 863-0223
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10592 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
```

```

: COUNTRY: U.S.A.
: ZIP: 80203
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/092,409
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/680,726
: FILING DATE: 12-JUL-1996
: ATTORNEY/AGENT INFORMATION:
: NAME: Connell, Gary J.
: REGISTRATION NUMBER: 32,020
: REFERENCE/DOCKET NUMBER: 2618-46-C1
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (303) 863-9700
: TELEFAX: (303) 863-0223
: INFORMATION FOR SEQ ID NO: 52:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 10592 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
US-09-092-409-52

Query Match 25.8%; Score 26.6; DB 3; Length 10592;
Best Local Similarity 60.3%; Pred. No. 15;
Matches 44; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

Oy 13 ATACAGTTATGACGACATTAAAGTCTCGATATGCAATTGCAATTAACGTTAA 72
Db 4826 AAAAAGTTCACGTCACATTGATGCTCCTACAGACTAGATTCTTACACCAATTCCA 4885
Oy 73 AAAACGGTATTTTC 85
Db 4886 TAAAGTTGGTTTC 4898

RESULT 35
US-09-702-705-655/c
: Sequence 655, Application US/09702705
: Patent No. 6504010
: GENERAL INFORMATION:
: APPLICANT: Wang, Tonglong
: APPLICANT: Bangur, Chaitanya S.
: APPLICANT: Lodges, Michael A.
: APPLICANT: Fanger, Gary
: APPLICANT: Vegdick, Tom
: APPLICANT: Carter, Darlick
: APPLICANT: Retter, Marc
: APPLICANT: Mannion, Jane
: APPLICANT: Fan, Liqun
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
: TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
: FILE REFERENCE: 210121.478C14
: CURRENT APPLICATION NUMBER: US/09/702,705
: CURRENT FILING DATE: 2000-10-30
: NUMBER OF SEQ ID NOS: 1833
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 655
: LENGTH: 494
: TYPE: DNA
: ORGANISM: Homo sapien
US-09-702-705-655

Query Match 25.6%; Score 26.4; DB 4; Length 494;
Best Local Similarity 65.0%; Pred. No. 8.2;
Matches 33; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

```

Qy 2 AAGTGACTGGAATAACAGTTAATGACAGCAATTAGCTCCGTGATGCGAATTGGCTA 61  
||||| | |||| | | ||||| ||||| | |||||  
Db 140 AAGTGAATTTATGATAGCTACATAAAGGAATTAAGAGCTCCTGCAGAGATTCCTTGGCGA 81

RESULT 36  
US-09-736

```

: Sequence 655, Application US/09736457
: Patent No. 6509448
:
: GENERAL INFORMATION:
:
: APPLICANT: Wang, Tongtong
: APPLICANT: Bangur, Chaitanya S.
: APPLICANT: Lodes, Michael A.
: APPLICANT: Fanger, Gary
: APPLICANT: Vedvyick, Tom
: APPLICANT: Carter, Darrick
: APPLICANT: Reltter, Marc
: APPLICANT: Mannion, Jane
: APPLICANT: Fan, Liqun
: APPLICANT: Wang, Aijun
:
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
: TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
:
: FILE REFERENCE: 210121.478C15
: CURRENT APPLICATION NUMBER: US/09/736,457
: CURRENT FILING DATE: 2000-12-13
:
: NUMBER OF SEQ ID NOS: 1864
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 655
: LENGTH: 494
:
: TYPE: DNA
: ORGANISM: Homo sapien
:
: US-09-736-457-655

```

Query Match	25.6%	Score	26.4	DB	4	Length	494
Best Local Similarity	65.0%	Pred.	No. 8.2				
Matches	39	Conservative	0	Mismatches	21	Indels	0
						Gaps	0

```

Oy      2  AAGTACTGGAATTAACAGTTTAAATGACAGCATTAACTCCTGCATATGTGAATTGCTA 61
        |||||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db     140 AAGTGAATTTTATGATAGCTACATAAAGCAATTAAAGAGCTCCTGCAGAGTTCCTTTGCCA 81

```

RESULT 37  
US-09-107

Sequence 3072, Application US/09107532A  
Patent No. 6583275  
GENERAL INFORMATION:  
APPLICANT: Lynn A Doucette-Stamm and David Bush  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO  
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS  
NUMBER OF SEQUENCES: 7310  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: GENOME THERAPEUTICS CORPORATION  
STREET: 100 Beaver Street  
CITY: Waltham  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02354  
COMPUTER READABLE FORM:  
MEDIUM TYPE: CD/ROM ISO9660  
COMPUTER: PC  
OPERATING SYSTEM: <Unknown>  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/107,532A  
FILING DATE: 30-Jun-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/085,598  
FILING DATE: 14 May 1998  
APPLICATION NUMBER: 60/051571  
FILING DATE: July 2, 1997  
ATTORNEY/AGENT INFORMATION:

NAME: Ariniello, Pamela Deneke  
REGISTRATION NUMBER: 40,489  
REFERENCE/DOCKET NUMBER: GTC-012  
TELECOMMUNICATION INFORMATION:

INFORMATION FOR SEQ ID NO: 3072  
SEQUENCE CHARACTERISTICS:

```

;
; LENGTH: 1293 base pairs
; TYPE: nucleic acid

```

```

; STRANDEDNESS: double
; TOPOLOGY: circular

```

```

; MOLECULE TYPE: DNA (genomic)
;
; HYPOTHETICAL: NO
;

```

ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORIGIN: Database

```

; ORGANISM: Enterococcus faecium
;
; FEATURE:
; NAME/KEY: t150 feature

```

NAME/KEY:	MISC_reacalc
LOCATION:	(B) LOCATION 1...1293
SEQUENCE DESCRIPTION:	SEQ ID NO: 3072

US-09-107-532A-3072

Query Match	25.48;	Score 26.2;	DB 4;	Length 1293;
Best Local Similarity	58.28;	Pred. NO. 12;		
Matches 46;	Conservative	0;	Mismatches 33;	Indels 0;
				Gaps 0;

OY 14 TAACAGTTTATGACAGCATTAATACCTCCATATGTGAATTGCTAATACAGTTAAAA 73  
 ||| | ||| | ||| ||| | ||| ||| | ||| |||  
 Db 573 TAAGAAAGATTGAAGAAGTGAAGACTCATCGAGAGCCGATCGCCCAAAAAAGAAAAA 632

QY	74	AAACG	TATTC	CC	TG	TT	92
Db	633	TAGC	GAGAT	TTT	TC	AGAT	651

RESULT 38  
US-09-647

```

: Sequence, Application US/09647826
: Patent No. 6437216
:
: GENERAL INFORMATION:
:
: APPLICANT: Duff, Gordon W.
: APPLICANT: Nicklin, Martin
: APPLICANT: Interleukin Genetics, Inc.
: TITLE OF INVENTION: TRANSGENIC MODELS OF INFLAMMATORY DISEASE
: FILE REFERENCE: MSA-003.01
: CURRENT APPLICATION NUMBER: US/09/647,826
: CURRENT FILING DATE: 2001-03-12
: PRIOR APPLICATION NUMBER: GB 972835.6
: PRIOR FILING DATE: 1997-11-13
: NUMBER OF SEQ ID NOS: 2
: SOFTWARE: PatentIn Ver. 2.0
:
: SEQ ID NO 1
:
: LENGTH: 6350
:
: TYPE: DNA
: ORGANISM: mouse
:
: US-09-647-826-1

```

Query Match	25.4%	Score	26.2	DB	4	Length	6350
Best Local Similarity	72.3%	Pred. No.	18				
Matches	34	Conservative	0	Mismatches	13	Indels	0
						Gaps	0

Qy 30 GCATTAAATAGCTCCTGCATAATGTGAATTGCTAATACAGTTAAAAAAA 76  
 . | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 Db 5216 GCAATTAGATGCTCCCTGCATTGTGTAATGGTATTAAAGCATAGAAGAAA 5262

RESULT 39  
US-09-996

```

; Sequence 105, Application US/09996243
; patent No. 6478825
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.

```

APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerltsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Guiney, Austin L.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C13  
CURRENT FILING DATE: 2001-11-14  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/065186  
PRIOR FILING DATE: 1997-11-12  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066770  
PRIOR FILING DATE: 1997-11-24  
PRIOR APPLICATION NUMBER: 60/075945  
PRIOR FILING DATE: 1998-02-25  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/083322  
PRIOR FILING DATE: 1998-04-28  
PRIOR APPLICATION NUMBER: 60/084600  
PRIOR FILING DATE: 1998-05-07  
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; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

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Query Match      25.28; Score 26; DB 4; Length 490;
Best Local Similarity 57.18; Pred. No. 11;
Matches 44; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

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QY      5 TGACGTGAATACAGCTTAATAGCCGATGATGTGATGCTATA 64
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QY      65 CAGTTAAAAACGGTA 81
      122 GCCTGTAATAAATANTTA 106
DB

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RESULT 40
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; Sequence 17, Application US/08616368A
; Patent No. 5767262
; GENERAL INFORMATION:
; APPLICANT: Lee, Mu-En
; APPLICANT: Haber, Edgar
; APPLICANT: Jain, Mukesh
; APPLICANT: Yet, Shaw-Fang

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; TITLE OF INVENTION: SMOOTH MUSCLE CELL LIM PROTEIN
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/616,368A
; FILING DATE: 15-MAR-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 05433/022001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ. ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 297 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-616-368a-17

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Query Match      25.08; Score 25.8; DB 1; Length 297;
Best Local Similarity 63.98; Pred. No. 11;
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RESULT 41
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; GENERAL INFORMATION:
; APPLICANT: Lee, Mu-En
; APPLICANT: Haber, Edgar
; APPLICANT: Jain, Mukesh
; APPLICANT: Yet, Shaw-Fang
; TITLE OF INVENTION: SMOOTH MUSCLE CELL LIM PROTEIN
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
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; SOFTWARE: FASTSEQ for Windows Version 2.0b
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; APPLICATION NUMBER: US/09/054,298

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: SEQUENCE CHARACTERISTICS:

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APPLICANT:

APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Matanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William T.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730PIC13  
CURRENT APPLICATION NUMBER: US/09/996,243  
PRIOR APPLICATION NUMBER: 2001-11-14  
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PRIOR APPLICATION NUMBER: 60/062250  
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PRIOR APPLICATION NUMBER: 60/090542

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; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

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Matches 45; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

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QY      65 CAGTTAAAAAAGGTA 81
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DB      200 GCCTGTAAAAAATAGTA 184
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; Patent No. 6478825
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Bolstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Foong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gertlisen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
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; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C13
; CURRENT APPLICATION NUMBER: US/09/996,243
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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Prior FILING DATE: 1998-07-02
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Prior FILING DATE: 1998-07-07
Prior APPLICATION NUMBER: 60/091982
Prior FILING DATE: 1998-07-07
Prior APPLICATION NUMBER: 60/092182
Prior FILING DATE: 1998-07-09
;

Query Match      25.0%; Score 25.8; DB 4; Length 552;
Best Local Similarity 58.4%; Pred. No. 13;
Matches 45; Conservative 0; Mismatches 32; Indels 0; Gaps 0

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QY      65 CAGTTAAAAAACGGTA 81
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Db      222 GCCGTAAAAAATAGTA 206
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Search completed: August 25, 2003, 07:50:31
Job time : 52 secs

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Search completed: August 25, 2003, 07:50:31
Job time : 52 secs
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Query Match	25.0%;	Score 25.8;	DB 4;	Length 552;
Best Local Similarity	58.4%;	Pred. No. 13;		
Matches 45;	Conservative 0;	Mismatches 32;	Indels 0;	Gaps 0

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C	1	36.7	35.1	74962	14	US-10-0274-974-3	Sequence 3, Appl
C	2	32	31.1	585	13	US-10-027-632-230735	Sequence 230735,
C	3	30.4	29.5	702	13	US-10-027-632-202236	Sequence 202236,
C	4	30.4	29.5	702	13	US-10-027-632-202237	Sequence 202237,
C	5	29.8	28.9	177556	11	US-09-952-213D-6	Sequence 6, Appl
C	6	29.6	28.7	533	13	US-10-027-632-245609	Sequence 245609,
C	7	29.4	28.5	31412	13	US-10-109-551-3	Sequence 3, Appl
C	8	29.2	28.3	585	13	US-10-027-632-320680	Sequence 320680,
C	9	29.2	28.3	1270	13	US-10-027-632-79603	Sequence 79603,
C	10	29.2	28.3	148567	10	US-09-801-8768-3	Sequence 3, Appl
C	11	29.2	28.3	148567	14	US-10-254-869-3	Sequence 3, Appl
C	12	29	28.2	687	13	US-10-027-632-11949	Sequence 11949,
C	13	28.8	28.0	1830121	14	US-10-329-960-1	Sequence 1, Appl
C	14	28.4	27.6	2692	14	US-10-114-170-215	Sequence 215, App
C	15	28	27.2	466	9	US-09-989-722-106	Sequence 106, App
C	16	28	27.2	466	9	US-09-989-722-106	Sequence 106, App

[illegible]

## ALIGNMENTS

RESULT 1  
US-10-274-974-3/c

; Sequence 3, Application US/1027  
; Publication No. US20030054490A1

```

; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al.

```

TITLE OF INVENTION: ISOLATED HUMAN PHOSPHATASE PROTEINS,  
NUCLEIC ACID MOLECULES ENCODING HUMAN PHOSPHATASE PROTEINS  
TITLE OF INVENTION:  
TITLE OF INVENTION:  
TITLE OF INVENTION:

; TITLE OF INVENTION: AND USES THEREOF  
 ; FILE REFERENCE: CL000871 DIV  
 ; COUNTRY AND INSTITUTION ORIGIN: US 410/324

```

; CURRENT APPLICATION NUMBER: 05/10/2002
; CURRENT FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: 00/695 853

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PRIOR APPLICATION NUMBER: 09/0885,853  
PRIOR FILING DATE: 2000-10-11  
PRIOR APPLICATION NUMBER: 60/183 184

PRIOR FILING DATE: 2000-02-14  
 NUMBER OF SEQ ID NOS: 3

```

7  NUMBER OF SEO ID NOS: 3
;  SOFTWARE: FastSEO for Windows Version 4.0
1  SEO ID NO 3

```

```

:
:
: LENGTH: 74962
:
: TYPE: DNA
:

```

ORGANISM: Homo sapiens  
FEATURE:

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; NAME/KEY: misc_feature
; LOCATION: (1)..(74962)

```

OTHER INFORMATION: n = A, T, C or G  
US-10-274-974-3

Query Match 35.1%; Score 36.2; DB 14; Length 74962

Best Local Similarity 62.9%; Pred. No. 0.89;  
Matches 56; Conservative 0; Mismatches 33; Indels 0; Gaps 0

12 AATAACAGTTTAAATGACAGCATTAATAGCTCCTGCATATGTGAATTGCTAATACAGTTAA 71

Db 63338 AAAAAAAAAAATTCAGCAATTCAAAGACCCCTAGAGACTTACTTTCTTAATCAATTAA 63275

72 AAAAACGTAATTCCCTGGTCTGATCCA 100

Db 63278 AAAAAGGCTTTTCAGTACTTCTCATCTA 63250

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RESULT 2
US-10-027-632-230735/c
; Sequence 230735, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 230735
; LENGTH: 585
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-230735

Query Match
Best Local Similarity 31.1%; Score 32; DB 13; Length 585;
Matches 56; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

QY 2 AAGTACTGGAATTAACAGATTATGACAGCATTAATAGCTCGATATGTAATGCTGA 61
DB 318 AATGATTTGCTTCACATTTTAAATTAACAAGGATTAAGCCCATATAAAGTTCTTACAA 259
QY 62 ATACAGTTAAAAAAGCGATTTCCTCGTCTGAT 97
DB 258 CAGAAGCTATTAATGTTTCCATCTTACTGAT 223

RESULT 3
US-10-027-632-202236/c
; Sequence 202236, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 202237
; LENGTH: 702
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-202237

Query Match
Best Local Similarity 29.5%; Score 30.4; DB 13; Length 702;
Matches 49; Conservative 0; Mismatches 31; Indels 0; Gaps 0;
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; SEQ ID NO 202236
; LENGTH: 702
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-202236

Query Match
Best Local Similarity 29.5%; Score 30.4; DB 13; Length 702;
Matches 49; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 11 GAATAACAGTTAATGACAGCATTAATAGCTCGATATGTAATGCTGAATGCTAATACAGTTA 70
DB 667 GGAGTACATTTTACATCTTTTATAGTTGTATATAAGAGATTGTAATAATACATTTA 608
QY 71 AAAAAACGATTTTCCCTGG 90
DB 607 AAAAAAATGTTTCCCTAG 588

RESULT 4
US-10-027-632-202237/c
; Sequence 202237, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 202237
; LENGTH: 702
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-202237

Query Match
Best Local Similarity 29.5%; Score 30.4; DB 13; Length 702;
Matches 49; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 11 GAATAACAGTTAATGACAGCATTAATAGCTCGATATGTAATGCTGAATGCTAATACAGTTA 70
DB 667 GGAGTACATTTTACATCTTTTATAGTTGTATATAAGAGATTGTAATAATACATTTA 608
QY 71 AAAAAACGATTTTCCCTGG 90
DB 607 AAAAAAATGTTTCCCTAG 588

RESULT 5
US-09-952-213D-6/c
; Sequence 6, Application US/09952213D
; Publication No. US20030096240A1
; GENERAL INFORMATION:
; APPLICANT: MURAD, FERID
; APPLICANT: SHARINA, IRAIDA G.
; APPLICANT: KRUMENACKER, J. S.
; APPLICANT: MARTIN, E.
```

```

; TITLE OF INVENTION: GENOMIC ORGANIZATION OF MOUSE AND HUMAN SGC
; FILE REFERENCE: USH:252US
; CURRENT APPLICATION NUMBER: US/09/952.213D
; CURRENT FILING DATE: 2002-08-16
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 177556
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (2293..144567)
; OTHER INFORMATION: N = A, C, T/U OR G
US-09-952-213D-6

Query Match      28.9%; Score 29.8; DB 11; Length 177556;
Best Local Similarity 56.7%; Pred. No. 1.1e+02;
Matches 55; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

OY      2  AACTGACTGGAATACAGTTTAATGACAGCATTAATGCTCCGATATGTGAATTGCTTA 61
Db      96352  AAGAGCATGAACATCTTCCATGACAGATCCATCGAATTCACAATTTGATGTC 96293

OY      62  ATACAGTTAAAAAAGCGTATTTCCCTGTTCTGATC 98
Db      96292  AAAAATTAAAGAAATCTTTTCTCTATCTTATC 96256

RESULT 6
US-10-027-632-245609
; Sequence 245609, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027.632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 245609
; LENGTH: 533
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-245609

Query Match      28.7%; Score 29.6; DB 13; Length 533;
Best Local Similarity 57.6%; Pred. No. 18;
Matches 53; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

OY      2  AACTGACTGGAATACAGTTTAATGACAGCATTAATGCTCCGATATGTGAATTGCTTA 61
Db      353  AAATAGCTGGATTACAGGTGTGGCCACCATGCTGGCTATGTGTGTGTGTTTA 412

OY      62  ATACAGTTAAAAAAGCGTATTTCCCTGTTCTGATC 93
Db      413  TTTTGTAGACAGATGAGGTGTTTGCATGTTTC 444
```

```

RESULT 7
US-10-109-551-3/C
; Sequence 3, Application US/10109551
; Publication No. US20020194635A1
; GENERAL INFORMATION:
; APPLICANT: DUNNE, PATRICK W.
; APPLICANT: PIEDRAHITA, JORGE
; TITLE OF INVENTION: TRANSGENIC ANIMALS RESISTANT TO TRANSMISSIBLE
; FILE REFERENCE: TAMK:207US
; CURRENT APPLICATION NUMBER: US/10/109.551
; CURRENT FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: 60/280,549
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 31412
; TYPE: DNA
; ORGANISM: Ovis aries
US-10-109-551-3

Query Match      28.5%; Score 29.4; DB 13; Length 31412;
Best Local Similarity 63.4%; Pred. No. 81;
Matches 45; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

OY      13  ATACAGTTTAATGACAGCATTAATGACTCTCTGCAATTCGTAATGCTTAATACAGTTAA 72
Db      21603  ATATCTGTTTAATGAAGAAATTAACATCTTCTGAAACATATTAATGCCACAGAAATTTTA 21544

OY      73  AAAAGGTATT 83
Db      21543  TCAAGGAATT 21533

RESULT 8
US-10-027-632-320680/C
; Sequence 320680, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027.632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 320680
; LENGTH: 585
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-320680

Query Match      28.3%; Score 29.2; DB 13; Length 585;
Best Local Similarity 62.2%; Pred. No. 25;
Matches 46; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

OY      30  GCATTAACTCTGCTGATATGTAATTCGCTAATACAGTTAAAAAAGCGTATTTCCCTG 89
```

DB 384 GCATTATACAGCTTCCAAATCCTAATGATTTGCTGACACAGGACTTTCACG 325  
QY 90 GTTCGATCCACA 103  
DB 324 GGTGTCATCAACA 311

## RESULT 9

US-10-027-632-79603/c  
; Sequence 79603, Application US/10027632  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; FILE REFERENCE: 108827.129  
; CURRENT APPLICATION NUMBER: US/10/027,632  
; PRIOR FILING DATE: 2002-04-30  
; PRIOR APPLICATION NUMBER: US 60/218,006  
; PRIOR FILING DATE: 2000-07-12  
; PRIOR APPLICATION NUMBER: US 60/198,676  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: US 60/193,483  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: US 60/185,218  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/167,363  
; PRIOR FILING DATE: 1999-11-23  
; PRIOR APPLICATION NUMBER: US 60/156,358  
; PRIOR FILING DATE: 1999-09-28  
; PRIOR APPLICATION NUMBER: US 60/146,002  
; PRIOR FILING DATE: 1998-08-09  
; NUMBER OF SEQ ID NOS: 325720  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 79603  
; LENGTH: 1270  
; TYPE: DNA  
; ORGANISM: Human  
US-10-027-632-79603

Query Match 28.3%; Score 29.2; DB 13; Length 1270;  
Best Local Similarity 62.2%; Pred. No. 33;  
Matches 46; Conservative 0; Mismatches 28; Indels 0; Gaps 0;  
QY 30 GCATTAAATGCTCTGCATATGTGTAATACAGTTAAAAACGGTATTTCCCTG 89  
DB 1063 GGATTAAATACAGCTTCCAAATCCTAATGATTTGCTGACACAGGACTTTCACG 1004  
QY 90 GTTCGATCCACA 103  
DB 1003 GGTGTCATCAACA 990

## RESULT 10

US-09-801-876B-3/c  
; Sequence 3, Application US/09801876B  
; Patent No. US20020127683A1  
; GENERAL INFORMATION:  
; APPLICANT: Ye, Jane et al  
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
; FILE REFERENCE: 108827.129  
; CURRENT APPLICATION NUMBER: US/09/801,876B  
; PRIOR FILING DATE: 2001-03-09  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 148567  
; TYPE: DNA  
; ORGANISM: Human  
; FEATURE:  
NAME/KEY: misc\_feature

; LOCATION: (1)...(148567)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-801-876B-3

Query Match 28.3%; Score 29.2; DB 10; Length 148567;  
Best Local Similarity 56.1%; Pred. No. 1.5e+02;  
Matches 55; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY 5 TGACGTGAATTAACAGTTTAATGACAGCATTATAGCTCCGATATGTGAATGTAATA 64  
DB 73685 TGCATTGCATTATATGTATATACACATTAAATTTCTTTTGGCTGATTCCTACT 73626

QY 65 CAGTTAAAAAACGGTATTTCCCTGCTGATCCAC 102  
DB 73625 AATTGAACAAAGAAATTTGTGCCCTGCTATTTCTAAC 73588

## RESULT 11

US-10-254-869-3/c  
; Sequence 3, Application US/10254869  
; Publication No. US20030027307A1  
; GENERAL INFORMATION:  
; APPLICANT: Ye, Jane et al  
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
; FILE REFERENCE: 108827.129  
; CURRENT APPLICATION NUMBER: US/10/254,869  
; PRIOR FILING DATE: 2002-09-26  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 148567  
; TYPE: DNA  
; ORGANISM: Human  
; FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)...(148567)  
OTHER INFORMATION: n = A,T,C or G  
US-10-254-869-3

Query Match 28.3%; Score 29.2; DB 14; Length 148567;  
Best Local Similarity 56.1%; Pred. No. 1.5e+02;  
Matches 55; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY 5 TGACGTGAATTAACAGTTTAATGACAGCATTATAGCTCCGATATGTGAATGTAATA 64  
DB 73685 TGCATTGCATTATATGTATATACACATTAAATTTCTTTTGGCTGATTCCTACT 73626

QY 65 CAGTTAAAAAACGGTATTTCCCTGCTGATCCAC 102  
DB 73625 AATTGAACAAAGAAATTTGTGCCCTGCTATTTCTAAC 73588

## RESULT 12

US-10-027-632-11949/c  
; Sequence 11949, Application US/10027632  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; FILE REFERENCE: 108827.129  
; CURRENT APPLICATION NUMBER: US/10/027,632  
; PRIOR FILING DATE: 2002-04-30  
; PRIOR APPLICATION NUMBER: US 60/218,006  
; PRIOR FILING DATE: 2000-07-12  
; PRIOR APPLICATION NUMBER: US 60/198,676  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: US 60/193,483  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: US 60/185,218  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/167,363

```

: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 11949
: LENGTH: 687
: TYPE: DNA
: ORGANISM: Human
US-10-027-632-11949

Query Match      28.2%; Score 29; DB 13; Length 687;
Best Local Similarity 62.0%; Pred. No. 30;
Matches 44; Conservative 1; Mismatches 26; Indels 0; Gaps 0;

QY      4 GTGACTGGAATACGATTATGACAGCATTATAGCTCTGCATATGTAATGCTAAT 63
Db      410 GTGACTGGAACAAAGACAGACAGACATTTAAGGCTTTTATGCTATATAGAAAT 351
QY      64 ACAGTTAAAA 74
Db      350 ATTGTAATTA 340

RESULT 13
US-10-329-960-1/c
: Sequence 1, Application US/10329960
: Publication No. US20030099277A1
: GENERAL INFORMATION:
: APPLICANT: Fleischmann et al.
: TITLE OF INVENTION: Nucleotide Sequence of the Haemophilus influenzae Rd Genome, Frag
: FILE REFERENCE: PB186P1
: CURRENT APPLICATION NUMBER: US/10/329,960
: PRIOR FILING DATE: 2003-01-02
: PRIOR APPLICATION NUMBER: US 09/643,990
: PRIOR FILING DATE: 2000-08-23
: PRIOR APPLICATION NUMBER: US 08/487,429
: PRIOR FILING DATE: 1995-06-07
: PRIOR APPLICATION NUMBER: US 08/426,787
: PRIOR FILING DATE: 1995-04-21
: NUMBER OF SEQ ID NOS: 1
: SOFTWARE: Patent version 3.1
: SEQ ID NO 1
: LENGTH: 1830121
: TYPE: DNA
: ORGANISM: Haemophilus influenzae
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (4747)..(4747)
: OTHER INFORMATION: n equals a, t, g or c
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (9921)..(9921)
: OTHER INFORMATION: n equals a, t, g or c
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (10150)..(10150)
: OTHER INFORMATION: n equals a, t, g or c
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (29298)..(29298)
: OTHER INFORMATION: n equals a, t, g or c
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (36543)..(36543)
: OTHER INFORMATION: n equals a, t, g or c
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (36551)..(36551)
: OTHER INFORMATION: n equals a, t, g or c
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: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (36636)..(36636)
: OTHER INFORMATION: n equals a, t, g or c
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (40808)..(40810)
: OTHER INFORMATION: n equals a, t, g or c
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (44416)..(44416)
: OTHER INFORMATION: n equals a, t, g or c
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (44905)..(44905)
: OTHER INFORMATION: n equals a, t, g or c
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (44975)..(44975)
: OTHER INFORMATION: n equals a, t, g or c
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (45593)..(45593)
: OTHER INFORMATION: n equals a, t, g or c
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (45732)..(45732)
: OTHER INFORMATION: n equals a, t, g or c
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (47036)..(47036)
: OTHER INFORMATION: n equals a, t, g or c
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (51334)..(51334)
: OTHER INFORMATION: n equals a, t, g or c
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (51602)..(51602)
: OTHER INFORMATION: n equals a, t, g or c
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (51786)..(51786)
: OTHER INFORMATION: n equals a, t, g or c
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (51805)..(51805)
: OTHER INFORMATION: n equals a, t, g or c
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (55369)..(55369)
: OTHER INFORMATION: n equals a, t, g or c
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (65309)..(65309)
: OTHER INFORMATION: n equals a, t, g or c
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (65313)..(65313)
: OTHER INFORMATION: n equals a, t, g or c
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (80024)..(80024)
: OTHER INFORMATION: n equals a, t, g or c
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (100091)..(100091)
: OTHER INFORMATION: n equals a, t, g or c
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (102696)..(102696)
: OTHER INFORMATION: n equals a, t, g or c
: FEATURE:
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: LOCATION: (150841) .. (150841)
: OTHER INFORMATION: n equals a, t, g or c
: FEATURE:
: NAME/KEY: misc.feature
: LOCATION: (152500) .. (152500)
: OTHER INFORMATION: n equals a, t, g or c
: FEATURE:
: NAME/KEY: misc.feature
: LOCATION: (152530) .. (152530)

Query Match      28.0%; Score 28.8; DB 14; Length 1830121;
Best Local Similarity 58.0%; Pred. No. 3.9e+02;
Matches 51; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY      13  ATACAGCTTATGACAGCATTAATAGCTCCTGCATATGTAATGCAATACGTTAA 72
      1541231  ATTAAGAGCTGCTTATTTCCATAATAGTAGTGCATGATATTTCCATTTTAT 1541172

QY      73  AAAACGGATATTCCCTGGTCTGCATCA 100
      1541171  AAAAATATAATTCCTCTATCTCATACCA 1541144

Db      1541171  AAAAATATAATTCCTCTATCTCATACCA 1541144

RESULT 14
US-10-114-170-215/c
: Sequence 215, Application US/10114170
: Publication No. US20030023075A1
: GENERAL INFORMATION:
: APPLICANT: Blattner, Frederick R.
: Burland, Valerie
: Perna, Nicole T.
: Plunkett, Guy
: Welch, Rod
: TITLE OF INVENTION: No. US20030023075A1el Sequences of E. coli O157
: NUMBER OF SEQUENCES: 265
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Quarles & Brady
: STREET: 1 South Plunkney Street
: CITY: Madison
: STATE: WI
: COUNTRY: US
: ZIP: 53701-2113
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette, 3.50 inch, 1.44MB storage
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Word Perfect 8.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/10/114,170
: FILING DATE: 01-Apr-2002
: CLASSIFICATION: <Unknown>
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 09/453,702
: FILING DATE: 03-DEC-1999
: APPLICATION NUMBER: 60/110,955
: FILING DATE: 04-DEC-1998
: ATTORNEY/AGENT INFORMATION:
: NAME: Seay, Nicholas J.
: REGISTRATION NUMBER: 27386
: REFERENCE/DOCKET NUMBER: 960296,95017
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (608) 251-5000
: TELEFAX: (608) 251-9166
: INFORMATION FOR SEQ ID NO: 215:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2692
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: SEQUENCE DESCRIPTION: SEQ ID NO: 215:
: US-10-114-170-215

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Query Match      27.6%  Score 28.4; DB 14; Length 2692;
Best Local Similarity 54.9%  Pred. No. 72;
Matches 56; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

QY      2  AAGTACTGGAATTAACGTTTAATGACAGCATTAATAGCCTCCATATGTGAATGCTA 61
      1  ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      1129  ACGGATGCGACATATATTTATTTGACGAATAAGAACTACGMAAAATGTTTCCTT 1070
      1  ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY      62  ATACAGTTAAAAAAGCGTATTTCCCTGTTCTGATCCACACA 103
      1  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db      1069  TTTTGACAAATATATAAACACTTATGGAAGATCGATTGACACA 1028
      1  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |

RESULT 15
US-09-989-722-106/c
; Sequence 106, Application US/09989722
; Patent No. US20020072067A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Bolstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Geider, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC63
; CURRENT APPLICATION NUMBER: US/09/989,722
; PRIOR FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/087106
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087609
; PRIOR FILING DATE: 1998-06-02
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; PRIOR APPLICATION NUMBER: 60/087827
; PRIOR FILING DATE: 1998-06-03
; PRIOR APPLICATION NUMBER: 60/088021
; PRIOR FILING DATE: 1998-06-04
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; PRIOR FILING DATE: 1998-06-04
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; PRIOR APPLICATION NUMBER: 60/089908
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/089947
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Query Match	27.28;	Score 28;	DB 9;	Length 466;
Best Local Similarity	59.78;	Pred. NO. 53;		
Matches 46;	Conservative 0;	Mismatches 31;	Indels 0;	Gaps 0

RESULT 16  
US-09-989-723-106/c

Sequence 106, Application US/09989723  
 Patent No. US20020072092A1  
 GENERAL INFORMATION:  
 APPLICANT: Ashkenazi, Avi J.  
 APPLICANT: Baker, Kevin P.  
 APPLICANT: Bolstein, David  
 APPLICANT: Desnoyers, Luc  
 APPLICANT: Eaton, Dan L.  
 APPLICANT: Ferrara, Napoleone  
 APPLICANT: Fong, Sherman  
 APPLICANT: Gerber, Hanspeter  
 APPLICANT: Gerritsen, Mary E.  
 APPLICANT: Goddard, Audrey  
 APPLICANT: Godowski, Paul J.  
 APPLICANT: Grimaldi, J. Christopher  
 APPLICANT: Guiney, Austin L.  
 APPLICANT: Kijavini, Ivar J.  
 APPLICANT: Napier, Mary A.  
 APPLICANT: Pan, James  
 APPLICANT: Paoni, Nicholas F.  
 APPLICANT: Roy, Margaret Ann  
 APPLICANT: Stewart, Timothy A.  
 APPLICANT: Tunas, Daniel  
 APPLICANT: Watanabe, Colin K.  
 APPLICANT: Williams, P. Mickey  
 APPLICANT: Wood, William I.  
 APPLICANT: Zhang, Zemin  
 TITLE OF INVENTION: Secretd and Transmembrane Polypeptides and Nucleic  
 FILE OF INVENTION: Acids Encoding the Same  
 FILE REFERENCE: P2730P1C62  
 CURRENT APPLICATION NUMBER: US/09/989,723  
 CURRENT FILING DATE: 2001-11-19  
 PRIOR APPLICATION NUMBER: 60/049787  
 PRIOR FILING DATE: 1997-06-16  
 PRIOR APPLICATION NUMBER: 60/062250  
 PRIOR FILING DATE: 1997-10-17  
 PRIOR APPLICATION NUMBER: 60/065186  
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 PRIOR FILING DATE: 1997-11-24  
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 PRIOR FILING DATE: 1998-02-25  
 PRIOR APPLICATION NUMBER: 60/078910  
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 PRIOR APPLICATION NUMBER: 60/083322  
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;; PRIOR FILING DATE: 1998-06-04  
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;; PRIOR FILING DATE: 1998-06-24  
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;; PRIOR FILING DATE: 1998-06-24  
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;; PRIOR FILING DATE: 1998-06-25  
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;; PRIOR FILING DATE: 1998-06-25  
;; PRIOR APPLICATION NUMBER: 60/090690  
;; PRIOR FILING DATE: 1998-06-25  
;; PRIOR APPLICATION NUMBER: 60/090694  
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;; PRIOR APPLICATION NUMBER: 60/090863  
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;; PRIOR APPLICATION NUMBER: 60/091360  
;; PRIOR FILING DATE: 1998-07-01  
;; PRIOR APPLICATION NUMBER: 60/091478  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091544  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091519  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091626  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091633  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091978  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/091982  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/092182  
;; PRIOR FILING DATE: 1998-07-09

Query Match 27.2%; Score 28; DB 9; Length 466;  
Best Local Similarity 59.7%; Pred. No. 53;  
Matches 46; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

0y 5 TGACTGGAATACGTTTATGACGATTAATGCTCCGTCATGTCGATTCCTAATA 64  
||||| || ||||| | ||||| ||||| | |||

Db 216 TGAGTGTGTTNAATCTTTCATGCTGGATAAATACAGCTCATATGATTAATCCACCA 157  
QY 65 CAGTTAAAAACGGTA 81  
Db 156 CCCTGTAAAAAATAGTA 140

RESULT 17  
US-09-989-279-106/c  
Sequence 106, Application US/09989279  
Patent No. US20020072496A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Bolstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gertlisen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P27301C56  
CURRENT FILING DATE: 2001-11-19  
PRIOR APPLICATION NUMBER: US/09/989,279  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/065186  
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PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-12  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066770  
PRIOR FILING DATE: 1997-11-24  
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PRIOR APPLICATION NUMBER: 60/088876  
PRIOR FILING DATE: 1998-06-11  
PRIOR APPLICATION NUMBER: 60/089105  
PRIOR FILING DATE: 1998-06-12  
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;; PRIOR FILING DATE: 1998-07-09

Query Match 27.2%; Score 28; DB 9; Length 466;  
Best Local Similarity 59.7%; Pred. No. 53;  
Matches 46; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

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OY 65 CAGTTAAAAAAGCGTA 81

Db 156 CCCTGTAATAAATAAGTA 140  
RESULT 18  
US-09-989-727-106/c  
; Sequence 106, Application US/09989727  
; Patent No. US20020072497A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerlitsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Goddard, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gunney, Austin L.  
; APPLICANT: Kijavlin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2730PIC65  
; CURRENT APPLICATION NUMBER: US/09/989,727  
; PRIOR APPLICATION NUMBER: 60/049787  
; PRIOR FILING DATE: 1997-06-16  
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PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

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OY	65	CAGTTAAAAAACGTA	81		
Db	156	CCCTGTTAAAAAATAGTA	140		

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; Sequence 106, Application US/09989731  
; Patent No. US20020103125A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gertsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kjaavn, Ivar J.  
; APPLICANT: Napier, Mary A.  
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; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2730P1C70  
; CURRENT APPLICATION NUMBER: US/09/989,731  
; CURRENT FILING DATE: 2001-11-20  
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;; PRIOR FILING DATE: 1998-07-07  
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;; PRIOR FILING DATE: 1998-07-07  
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;; PRIOR FILING DATE: 1998-07-09

Query Match 27.2%; Score 28; DB 10; Length 466;  
Best Local Similarity 59.7%; Pred. No. 53;  
Matches 46; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 5 TGACTGAAATACAGTTTATGACAGCATTATAGCTTCGTCATATGTAATGCTATA 64  
DB 216 TGACTGCTTAAATCTTCAATGCGATATAATACAGCTGCATCTATGATAATCCACCA 157  
QY 65 CAGTTAAAAAACGTA 81  
DB 156 CCCTGTAATAAATAGTA 140

RESULT 20  
US-09-989-732-106/c

;; Sequence 106, Application US/09989732  
;; Patent No. US20020123463A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Ashkenazi, Avi J.  
;; APPLICANT: Baker, Kevin P.  
;; APPLICANT: Botstein, David  
;; APPLICANT: Desnoyers, Luc  
;; APPLICANT: Eaton, Dan L.  
;; APPLICANT: Ferrara, Napoleone  
;; APPLICANT: Fong, Sherman  
;; APPLICANT: Gerber, Hanspeter  
;; APPLICANT: Gertitsen, Mary E.  
;; APPLICANT: Goddard, Audrey  
;; APPLICANT: Godowski, Paul J.  
;; APPLICANT: Grimaldi, J. Christopher  
;; APPLICANT: Gurney, Austin L.  
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;; APPLICANT: Napier, Mary A.  
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;; APPLICANT: Roy, Margaret Ann  
;; APPLICANT: Stewart, Timothy A.  
;; APPLICANT: Tumas, Daniel  
;; APPLICANT: Watanabe, Colin K.  
;; APPLICANT: Williams, P. Mickey  
;; APPLICANT: Wood, William I.  
;; APPLICANT: Zhang, Zemin  
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
;; FILE REFERENCE: P2730PIC57  
;; CURRENT FILING DATE: 2001-11-19  
;; PRIOR APPLICATION NUMBER: 60/049787  
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PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match 27.2% Score 28; DB 10; Length 466;  
Best Local Similarity 59.7%; Pred. No. 53;  
Matches 46; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

OY 5 TGACTGGAATAACGTTTAATGACAGCATTAATAGCTCCTGATATGTAATGCTAATA 64  
DB 216 TGAGTGGTTNAAATCTTTACATGCGTGGAATAATAACAGCTGATGATATATCCACCA 157  
OY 65 CAGTTAAAAAAGCGTA 81  
DB 156 CCGCTGTAATAAATAGTA 140

RESULT 21  
US-09-991-073-106/c  
; Sequence 106, Application US/09991073  
; Patent No. US20020127576A1  
; GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnuyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gertlisen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kijaviri, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730PIC15  
CURRENT APPLICATION NUMBER: US/09/991,073  
CURRENT FILING DATE: 2001-11-14  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
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;; PRIOR FILING DATE: 1998-06-24  
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;; PRIOR FILING DATE: 1998-07-09

Query Match 27.2%; Score 28; DB 10; Length 466;  
Best Local Similarity 59.7%; Pred. No. 53;  
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OY 5 TGACGTGAATACAGCTTAATGACAGCATTAATAGCTCCGCATATGTGAATTCCTAATA 64  
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DB 156 CCGCTGTAAAAAATAGTA 140

RESULT 22  
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; Sequence 106, Application US/09990442  
; Patent No. US20020132252A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David

;; APPLICANT: Desnoyers, Luc  
;; APPLICANT: Eaton, Dan L.  
;; APPLICANT: Ferrara, Napoleone  
;; APPLICANT: Fong, Sherman  
;; APPLICANT: Gerber, Hanspeter  
;; APPLICANT: Gerritsen, Mary E.  
;; APPLICANT: Goddard, Audrey  
;; APPLICANT: Godowski, Paul J.  
;; APPLICANT: Grimaldi, J. Christopher  
;; APPLICANT: Gunney, Austin L.  
;; APPLICANT: Kijavlin, Ivar J.  
;; APPLICANT: Napier, Mary A.  
;; APPLICANT: Pan, James  
;; APPLICANT: Paoni, Nicholas F.  
;; APPLICANT: Roy, Margaret Ann  
;; APPLICANT: Stewart, Timothy A.  
;; APPLICANT: Tumas, Daniel  
;; APPLICANT: Watanabe, Colin K.  
;; APPLICANT: Williams, P. Mickey  
;; APPLICANT: Wood, William I.  
;; APPLICANT: Zhang, Zemin  
;; TITLE OR INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
;; FILE REFERENCE: P2730P1C8  
;; CURRENT APPLICATION NUMBER: US/09/990,442  
;; CURRENT FILING DATE: 2001-11-14  
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PRIOR FILING DATE: 1998-07-07  
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PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match 27.2%; Score 28; DB 10; Length 466;  
Best Local Similarity 59.7%; Pred. No. 53;  
Matches 46; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 5 TGACGGAATACACTTTAATGACGACATTAATAGCTCTCGATATGGAATGCTAATA 64  
DB 216 TTAGGCTTAAATCTTCATGCTGGATAAATACAGCTGATCTAATGATACACCA 157  
QY 65 CAGTTAAAAAAGCGTA 81  
DB 156 CCCTGTAATAAATAGTA 140

RESULT 23  
US-09-991-163-106/c  
Sequence 106, Application US/09991163  
Patent No. US20020132253A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone

APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerltsen, Mary E.  
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APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C17  
CURRENT APPLICATION NUMBER: US/09/991,163  
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;; PRIOR FILING DATE: 1998-07-09

Query Match 27.2%; Score 28; DB 10; Length 466;  
Best Local Similarity 59.7%; Pred No 53;  
Matches 46; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

OY 5 TGACTGGAATAACAGTTTAATGACGATTAATAGCTCTCGCATATGTAATGCTAATA 64  
Db 216 TGAGGCGTTNAATCTTCATGCGGATTAATAACAGCTGATCTATGATATACACCA 157

OY 65 CAGTAAAAAACGTA 81  
Db 156 CCGTGAATAAATAAGTA 140

RESULT 24

US-09-993-604-106/c  
Sequence 106; Application US/0993604  
Patent No. US20020137075A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Bolstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrare, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerlitsen, Mary E.

;; APPLICANT: Goddard, Audrey  
;; APPLICANT: Godowski, Paul J.  
;; APPLICANT: Grimaldi, J. Christopher  
;; APPLICANT: Guiney, Austin L.  
;; APPLICANT: Kjlavin, Ivar J.  
;; APPLICANT: Napier, Mary A.  
;; APPLICANT: Pan, James  
;; APPLICANT: Paoni, Nicholas F.  
;; APPLICANT: Roy, Margaret Ann  
;; APPLICANT: Stewart, Timothy A.  
;; APPLICANT: Tumas, Daniel  
;; APPLICANT: Watanabe, Colin K.  
;; APPLICANT: Williams, P. Mickey  
;; APPLICANT: Wood, William I.  
;; APPLICANT: Zhang, Zemin  
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
;; FILE REFERENCE: P2730PIC25  
;; CURRENT FILING DATE: 2001-11-14  
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OY 65 CAGTTAAAAAAGCGTA 81  
DB 156 CCGGTAAAAAATAGTA 140

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Sequence 106, Application US/09990456  
Patent No. US20020137890A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
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APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin L.  
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APPLICANT: Pan, James  
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APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
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PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match 27.24; Score 28; DB 10; Length 466;

Best Local Similarity 59.7%; Pred. No. 53;

Matches 46; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

OY 5 TGACTGCATTAACAGTTTAATGACAGCATTAAAGTCTGCATATGTGAATGCTATA 64  
DB 216 TGAGTGGTTTAAATCTTTGATGCGGTAATAACAGCTGATCATATGATATCCACCA 157  
OY 65 CAGTTAAAAAAGCGTA 81  
DB 156 CCCTGTAATAAATAGTA 140

RESULT 26

US-09-989-721-106/c

; Sequence 106, Application US/09989721

; Patent No. US20020142961A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerlitsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Kijavyn, Ivar J.

; APPLICANT: Napier, Mary A.

APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Matanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C55  
CURRENT FILING DATE: US/09/989,721  
PRIOR FILING DATE: 2001-11-19  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
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PRIOR FILING DATE: 1998-07-07  
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PRIOR FILING DATE: 1998-07-09

Query Match 27.2%; Score 28; DB 10; Length 466;  
Best Local Similarity 59.7%; Pred. No. 53;  
Matches 46; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

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DB 216 TGAGTGTGTTAAATCTTCATGCTGAGTAATAATACAGCTGATCTATGATTAATACACA 157  
QY 65 CAGTTAAAAAAGCGTA 81  
DB 156 CCCTGTAATAAATAGTA 140

RESULT 27  
US-09-992-598-106/c  
Sequence 106, Application US/09992598  
Patent No. US20020160384A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gottlieb, Mary E.  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann

APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Matanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2730PIC20  
CURRENT APPLICATION NUMBER: US/09/992,598  
CURRENT FILING DATE: 2001-11-14  
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PRIOR FILING DATE: 1998-06-24  
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PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090557  
PRIOR FILING DATE: 1998-06-24  
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: PRIOR FILING DATE: 1998-06-25
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: PRIOR FILING DATE: 1998-07-09

Query Match          27.2%  Score 28; DB 10; Length 466;
Best Local Similarity 59.7%  Pred No. 53;
Matches 46; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 5 TGACTGGAATACAGCTTTAATGACAGCATTTATAGCTCTCGCATGTGGAATGCTAATA 64
Db 216 TGAGCGCTTNAATCTTCATGCTGATTAATAACAGCTGCATCTATGATTAATGCACCA 157
QY 65 CAGTTAAAAAACGCTA 81
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RESULT 28
US-09-989-293A-106/C
: Sequence 106, Application US/09989293A
: Patent No. US20020177164A1
: GENERAL INFORMATION:
: APPLICANT: Ashkenazi, Avi J.
: APPLICANT: Baker, Kevin P.
: APPLICANT: Botstein, David
: APPLICANT: Desnovers, Luc
: APPLICANT: Eaton, Dan L.
: APPLICANT: Ferrara, Napoleone
: APPLICANT: Fong, Sherman
: APPLICANT: Gerber, Hanspeter
: APPLICANT: Gerritsen, Mary E.
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Grimaldi, J. Christopher
: APPLICANT: Gurney, Austin L.
: APPLICANT: Kijavlin, Ivar J.
: APPLICANT: Napier, Mary A.
: APPLICANT: Pan, James
: APPLICANT: Paonli, Nicholas F.
: APPLICANT: Roy, Margaret Ann
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Watanabe, Colin K.
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: APPLICANT: Williams, P. Mickey
: APPLICANT: Wood, William I.
: APPLICANT: Zhang, Zemin
: TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
: FILE REFERENCE: P2730PIC66
: CURRENT FILING DATE: 2001-11-20
: PRIOR APPLICATION NUMBER: 60/049787
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;; PRIOR FILING DATE: 1998-06-25

;; PRIOR APPLICATION NUMBER: 60/090690  
;; PRIOR FILING DATE: 1998-06-25  
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;; PRIOR APPLICATION NUMBER: 60/090863  
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;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091978  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/091982  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/092182  
;; PRIOR FILING DATE: 1998-07-09

Query Match 27.2%; Score 28; DB 10; Length 466;  
Best Local Similarity 59.7%; Pred. No. 53;  
Matches 46; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 5 TGAAGTGAATACAGCATTAAATAGCTCTGCATATGTGTAATTCCTATA 64  
DB 216 TGAAGTGTGTNAACCTTCAATGCGGATTAATACAGCTGCATCTGTGTAATCCACCA 157  
QY 65 CAGTTAAAAAACGCTA 81  
DB 156 CCGTGTAAAAAATAGTA 140

RESULT 29  
US-09-989-735-106/c  
; Sequence 106, Application US/09989735  
; Publication No. US20020193299A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kijavini, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730PIC61  
CURRENT FILING DATE: 2001-11-19  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
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PRIOR FILING DATE: 1997-11-12  
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PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066770  
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PRIOR FILING DATE: 1998-02-25  
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PRIOR FILING DATE: 1998-04-28  
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PRIOR FILING DATE: 1998-06-11

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PRIOR FILING DATE: 1998-06-25  
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PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match 27.2%; Score 28; DB 10; Length 466;  
Best Local Similarity 59.7%; Pred. No. 53;  
Matches 46; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 5 TGACGTGAATAACAGTTATGACAGATTAATAGCTCCGCAATGTGATTCCTATA 64  
DB 216 TGAGTGGTTAAATCTTTCATGCTGGATAAATAACAGTCATCTATGTAATCCACCA 157  
QY 65 CAGTTAAAAAACGTA 81  
DB 156 CCCTGTAAAAAATAGTA 140

RESULT 30  
US-09-990-444-106/C  
Sequence 106, Application US/09990444  
Publication No. US20020193300A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnovers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Feng, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerlitsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Pao, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Matanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2730P1C19

CURRENT APPLICATION NUMBER: US/09/990,444  
CURRENT FILING DATE: 2001-11-14  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
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PRIOR APPLICATION NUMBER: 60/066770  
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PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088858  
PRIOR FILING DATE: 1998-06-11  
PRIOR APPLICATION NUMBER: 60/088861  
PRIOR FILING DATE: 1998-06-11  
PRIOR APPLICATION NUMBER: 60/088876





[illegible]

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: PRIOR FILING DATE: 1998-06-26
: PRIOR APPLICATION NUMBER: 60/090863
: PRIOR FILING DATE: 1998-06-26
: PRIOR APPLICATION NUMBER: 60/091360
: PRIOR FILING DATE: 1998-07-01
: PRIOR APPLICATION NUMBER: 60/091478
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: PRIOR APPLICATION NUMBER: 60/091626
: PRIOR FILING DATE: 1998-07-02
: PRIOR APPLICATION NUMBER: 60/091633
: PRIOR FILING DATE: 1998-07-02
: PRIOR APPLICATION NUMBER: 60/091978
: PRIOR FILING DATE: 1998-07-07
: PRIOR APPLICATION NUMBER: 60/091982
: PRIOR FILING DATE: 1998-07-07
: PRIOR APPLICATION NUMBER: 60/092182
: PRIOR FILING DATE: 1998-07-09
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Query Match          27.2%; Score 28; DB 10; Length 466;
Best Local Similarity 59.7%; Pred. No. 53;
Matches 46; Conservative 0; Mismatches 31; Indels 0; Gaps 0;
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QY      5 TCACGCGATACAGTTTATGACAGCATTAATAGCTCCTGCATATGTAATGCTAATA 64
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Db      216 TGAGTGGTTAATATCTTTCATGTGTGGATTAATACAGCTGCATATGTAATGCCACCA 157
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      65 CAGTTAAAAAAGCGTA 81
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      156 CCGCTGAAAAAATAGTA 140
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RESULT 32
US-09-989-730-106/c
: Sequence 106, Application US/09989730
: Publication No. US20020197674A1
: GENERAL INFORMATION:
: APPLICANT: Ashkenazi, Avi J.
: APPLICANT: Baker, Kevin P.
: APPLICANT: Botstein, David
: APPLICANT: Desnoyers, Luc
: APPLICANT: Eaton, Dan L.
: APPLICANT: Ferrara, Napoleone
: APPLICANT: Fong, Sherman
: APPLICANT: Gerber, Hanspeter
: APPLICANT: Gottlisen, Mary E.
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Grimaldi, J. Christopher
: APPLICANT: Guiney, Austin L.
: APPLICANT: Kiljavin, Ivar J.
: APPLICANT: Napier, Mary A.
: APPLICANT: Pan, James
: APPLICANT: Paoni, Nicholas F.
: APPLICANT: Roy, Margaret Ann
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Williams, Colin K.
: APPLICANT: Williams, P. Mickey
: APPLICANT: Wood, William I.
: APPLICANT: Zhang, Zemin
: TITLE OF INVENTION: Sectioned and Transmembrane Polypeptides and Nucleic
: FILE REFERENCE: P2730P1C69
: CURRENT APPLICATION NUMBER: US/09/989,730
: PRIOR FILING DATE: 2001-11-20
: PRIOR APPLICATION NUMBER: 60/049787
: PRIOR FILING DATE: 1997-06-16
: PRIOR APPLICATION NUMBER: 60/062250
: PRIOR FILING DATE: 1997-10-17
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: PRIOR APPLICATION NUMBER: 60/065186
: PRIOR FILING DATE: 1997-11-12
: PRIOR APPLICATION NUMBER: 60/065311
: PRIOR FILING DATE: 1997-11-13
: PRIOR APPLICATION NUMBER: 60/066770
: PRIOR FILING DATE: 1997-11-24
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: PRIOR APPLICATION NUMBER: 60/083322
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1      PRIOR APPLICATION NUMBER: 60/091360
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10     PRIOR FILING DATE: 1998-07-02
11     PRIOR APPLICATION NUMBER: 60/091633
12     PRIOR FILING DATE: 1998-07-02
13     PRIOR APPLICATION NUMBER: 60/091978
14     PRIOR FILING DATE: 1998-07-07
15     PRIOR APPLICATION NUMBER: 60/091982
16     PRIOR FILING DATE: 1998-07-07
17     PRIOR APPLICATION NUMBER: 60/092182
18     PRIOR FILING DATE: 1998-07-09
19
20 Query Match      27.2%; Score 28; DB 10; Length 466;
21 Best Local Similarity 59.7%; Pred. No. 53;
22 Matches 46; Conservative 0; Mismatches 31; Indels 0; Gaps 0
23
24 QY      5 TGACGTGGAATAACACTTTAATGACACGCAATTATAGCTCTGCGATATGCAATTCGTAATA 64
25         ||| ||| || ||| ||| || ||| || ||| ||| ||| ||| ||| ||| ||| |||
26 Db      216 TGAGGGGTGTTAAATCTTCATGCTGGATGAATAAATACAGCTGATCTATGATATATCCACCA 157
27         || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
28
29 Db      156 CCTGTGTAATAAATACTA 140
30
31 RESULT 33
32 US-09-990-436-106/c
33 Sequence 106, Application US/09990436
34 Publication No. US20020198148A1
35
36 GENERAL INFORMATION:
37
38 APPLICANT: Ashkenazi, Avi J.
39 APPLICANT: Baker, Kevin P.
40 APPLICANT: Botstein, David
41 APPLICANT: Deenoyers, Luc
42 APPLICANT: Eaton, Dan L.
43 APPLICANT: Ferrara, Napoleone
44 APPLICANT: Fong, Sherman
45 APPLICANT: Gerber, Hanspeter
46 APPLICANT: Gerritsen, Mary E.
47 APPLICANT: Goddard, Audrey
48 APPLICANT: Godowski, Paul J.
49 APPLICANT: Grimaldi, J. Christopher
50 APPLICANT: Gurney, Austin L.
51 APPLICANT: Kljavin, Ivar J.
52 APPLICANT: Napier, Mary A.
53 APPLICANT: Pan, James
54 APPLICANT: Paoni, Nicholas F.
55 APPLICANT: Roy, Margaret Ann
56 APPLICANT: Stewart, Timothy A.
57 APPLICANT: Tumas, Daniel
58 APPLICANT: Watanabe, Colin K.
59 APPLICANT: Williams, P. Mickey
60 APPLICANT: Wood, William I.
61 APPLICANT: Zhang, Zemin
62
63 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
64 FILE REFERENCE: P2730P1C14
65 CURRENT FILING DATE: US/09/990,436
66 PRIOR APPLICATION NUMBER: 60/049787
67 PRIOR FILING DATE: 1997-06-16
68 PRIOR APPLICATION NUMBER: 60/062250
69 PRIOR FILING DATE: 1997-10-17
70 PRIOR APPLICATION NUMBER: 60/065186
71 PRIOR FILING DATE: 1997-11-12
72 PRIOR APPLICATION NUMBER: 60/065311

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[illegible]

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; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091544
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091626
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match      27.2%; Score 28; DB 10; Length 466;
Best Local Similarity 59.7%; Pred. No. 53;
Matches 46; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY      5  TCACGTGCAATACAGTTTATGACACGATTATAGCTCCGCAATGTCGATTGCTATATA 64
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      216  TCGGTGGTTAAATCTTTCATGCTGGATTAACAGCTGCATCATGATTAATCCACCA 157
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      65  CAGTTAAAAAACGTA 81
          | | ||||| |||
Db      156  CCCTGTAATAAATAGTA 140
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 34
US-09-993-687-106/c
; Sequence 106, Application US/09993687
; Publication No. US20020198149A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gertlisen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C11
; CURRENT APPLICATION NUMBER: US/09/993,687
; CURRENT FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
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; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/087106
; PRIOR FILING DATE: 1998-05-28
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; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087609
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087759
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087827
; PRIOR FILING DATE: 1998-06-03
; PRIOR APPLICATION NUMBER: 60/088021
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088025
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088026
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088028
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088029
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088030
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088033
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088326
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; PRIOR APPLICATION NUMBER: 60/088167
; PRIOR FILING DATE: 1998-06-05
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; PRIOR FILING DATE: 1998-06-09
; PRIOR APPLICATION NUMBER: 60/088734
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088738
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088742
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; PRIOR APPLICATION NUMBER: 60/088810
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088824
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; PRIOR APPLICATION NUMBER: 60/088826
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; PRIOR APPLICATION NUMBER: 60/089514
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; PRIOR APPLICATION NUMBER: 60/089532
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089538
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;; PRIOR FILING DATE: 1998-06-17  
;; PRIOR APPLICATION NUMBER: 60/089598  
;; PRIOR FILING DATE: 1998-06-17  
;; PRIOR APPLICATION NUMBER: 60/089599  
;; PRIOR FILING DATE: 1998-06-17  
;; PRIOR APPLICATION NUMBER: 60/089600  
;; PRIOR FILING DATE: 1998-06-17  
;; PRIOR APPLICATION NUMBER: 60/089653  
;; PRIOR FILING DATE: 1998-06-17  
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;; PRIOR FILING DATE: 1998-06-18  
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;; PRIOR APPLICATION NUMBER: 60/090349  
;; PRIOR FILING DATE: 1998-06-23  
;; PRIOR APPLICATION NUMBER: 60/090355  
;; PRIOR FILING DATE: 1998-06-23  
;; PRIOR APPLICATION NUMBER: 60/090429  
;; PRIOR FILING DATE: 1998-06-24  
;; PRIOR APPLICATION NUMBER: 60/090431  
;; PRIOR FILING DATE: 1998-06-24  
;; PRIOR APPLICATION NUMBER: 60/090435  
;; PRIOR FILING DATE: 1998-06-24  
;; PRIOR APPLICATION NUMBER: 60/090444  
;; PRIOR FILING DATE: 1998-06-24  
;; PRIOR APPLICATION NUMBER: 60/090445  
;; PRIOR FILING DATE: 1998-06-24  
;; PRIOR APPLICATION NUMBER: 60/090472  
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;; PRIOR FILING DATE: 1998-06-24  
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;; PRIOR FILING DATE: 1998-06-24  
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;; PRIOR FILING DATE: 1998-06-25  
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;; PRIOR FILING DATE: 1998-06-25  
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;; PRIOR FILING DATE: 1998-06-26  
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;; PRIOR FILING DATE: 1998-06-26  
;; PRIOR APPLICATION NUMBER: 60/091360  
;; PRIOR FILING DATE: 1998-07-01  
;; PRIOR APPLICATION NUMBER: 60/091478  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091544  
;; PRIOR FILING DATE: 1998-07-01

;; PRIOR APPLICATION NUMBER: 60/091519  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091626  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091633  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091978  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/091982  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/092182  
;; PRIOR FILING DATE: 1998-07-09

Query Match 27.2%; Score 28; DB 10; Length 466;  
Best Local Similarity 59.7%; Pred. No. 53;  
Matches 46; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 5 TGACGTGATTAACAGTTTATATGACAGCATTAATAGCTCTCGATATGTAATTGCTTAATA 64  
DB 216 TGAGTGGTTTAAATCTTCATGATGGGATTAATACAGCTGATATGATATCCACCA 157  
QY 65 CAGTTAAAAAACGGTA 81  
DB 156 CCCTGTAATAATAGTA 140

RESULT 35  
US-09-989-734-106/c  
; Sequence 106, Application US/09989734  
; Publication No. US20030003531A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, T. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2730P1C64  
; CURRENT APPLICATION NUMBER: US/09/989,734  
; PRIOR APPLICATION NUMBER: 60/049787  
; PRIOR FILING DATE: 1997-06-16  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/065186  
; PRIOR FILING DATE: 1997-11-12  
; PRIOR APPLICATION NUMBER: 60/065311  
; PRIOR FILING DATE: 1997-11-13  
; PRIOR APPLICATION NUMBER: 60/066770  
; PRIOR FILING DATE: 1997-11-24  
; PRIOR APPLICATION NUMBER: 60/075945  
; PRIOR FILING DATE: 1998-02-25  
; PRIOR APPLICATION NUMBER: 60/078910

PRIOR APPLICATION NUMBER: 60/089599	PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089600	PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089601	PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089653	PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089801	PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089907	PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089948	PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089952	PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/090246	PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090252	PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090254	PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090431	PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090435	PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090444	PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090445	PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090472	PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090535	PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090540	PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090542	PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090557	PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090676	PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090678	PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090650	PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090656	PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090659	PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090655	PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090636	PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090822	PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/090853	PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/091360	PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091478	PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091544	PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519	PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626	PRIOR FILING DATE: 1998-07-02

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; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match      27.2%; Score 28; DB 11; Length 466;
Best Local Similarity 59.7%; Pred. No. 53;
Matches 46; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY      5 TCACGCGATACAGTTTATGACAGCATTAATAGCTCCTGCATATGTAATGCTAATA 64
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      216 TGAGGTGTTAATCTTTTCATGTGGGATTAATACAGCTGCATCATATATCCACCA 157
        | | ||| ||| |||

QY      65 CAGTTAAAAACGGTA 81
        | | ||| ||| |||
Db      156 CCCCTGTAATAATAATAGTA 140

RESULT 36
US-09-997-653-106/c
; Sequence 106, Application US/09997653
; Publication No. US20030008297A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Getzler, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: K1 Javlin, Ivar J.
; APPLICANT: Knapler, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C38
; CURRENT APPLICATION NUMBER: US/09/997,653
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
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; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/087106
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087609
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; PRIOR APPLICATION NUMBER: 60/087827
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; PRIOR APPLICATION NUMBER: 60/088021
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; PRIOR APPLICATION NUMBER: 60/088026
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088028
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; PRIOR APPLICATION NUMBER: 60/089599
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089600
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;; PRIOR FILING DATE: 1998-06-17  
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;; PRIOR APPLICATION NUMBER: 60/089801  
;; PRIOR FILING DATE: 1998-06-18  
;; PRIOR APPLICATION NUMBER: 60/089907  
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;; PRIOR APPLICATION NUMBER: 60/089947  
;; PRIOR FILING DATE: 1998-06-19  
;; PRIOR APPLICATION NUMBER: 60/089948  
;; PRIOR FILING DATE: 1998-06-19  
;; PRIOR APPLICATION NUMBER: 60/089952  
;; PRIOR FILING DATE: 1998-06-19  
;; PRIOR APPLICATION NUMBER: 60/090246  
;; PRIOR FILING DATE: 1998-06-22  
;; PRIOR APPLICATION NUMBER: 60/090252  
;; PRIOR FILING DATE: 1998-06-22  
;; PRIOR APPLICATION NUMBER: 60/090254  
;; PRIOR FILING DATE: 1998-06-22  
;; PRIOR APPLICATION NUMBER: 60/090349  
;; PRIOR FILING DATE: 1998-06-23  
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;; PRIOR FILING DATE: 1998-06-23  
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;; PRIOR FILING DATE: 1998-06-24  
;; PRIOR APPLICATION NUMBER: 60/090431  
;; PRIOR FILING DATE: 1998-06-24  
;; PRIOR APPLICATION NUMBER: 60/090435  
;; PRIOR FILING DATE: 1998-06-24  
;; PRIOR APPLICATION NUMBER: 60/090444  
;; PRIOR FILING DATE: 1998-06-24  
;; PRIOR APPLICATION NUMBER: 60/090445  
;; PRIOR FILING DATE: 1998-06-24  
;; PRIOR APPLICATION NUMBER: 60/090472  
;; PRIOR FILING DATE: 1998-06-24  
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;; PRIOR FILING DATE: 1998-06-24  
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;; PRIOR FILING DATE: 1998-06-24  
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;; PRIOR APPLICATION NUMBER: 60/090557  
;; PRIOR FILING DATE: 1998-06-24  
;; PRIOR APPLICATION NUMBER: 60/090676  
;; PRIOR FILING DATE: 1998-06-25  
;; PRIOR APPLICATION NUMBER: 60/090678  
;; PRIOR FILING DATE: 1998-06-25  
;; PRIOR APPLICATION NUMBER: 60/090690  
;; PRIOR FILING DATE: 1998-06-25  
;; PRIOR APPLICATION NUMBER: 60/090694  
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;; PRIOR APPLICATION NUMBER: 60/090695  
;; PRIOR FILING DATE: 1998-06-25  
;; PRIOR APPLICATION NUMBER: 60/090696  
;; PRIOR FILING DATE: 1998-06-25  
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;; PRIOR APPLICATION NUMBER: 60/090863  
;; PRIOR FILING DATE: 1998-06-26  
;; PRIOR APPLICATION NUMBER: 60/091360  
;; PRIOR FILING DATE: 1998-07-01  
;; PRIOR APPLICATION NUMBER: 60/091478  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091544  
;; PRIOR FILING DATE: 1998-07-01  
;; PRIOR APPLICATION NUMBER: 60/091519  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091626  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091633  
;; PRIOR FILING DATE: 1998-07-02

;; PRIOR APPLICATION NUMBER: 60/091978  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/091982  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/092182  
;; PRIOR FILING DATE: 1998-07-09

Query Match 27.2% Score 28; DB 11; Length 466;  
Best Local Similarity 59.7% Pred. No. 53;  
Matches 46; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

Qy 5 TGAAGTGAATACAGCTTAATGACGATTAATGCTCCGATATGGAATGCTATA 64  
Db 216 TGAAGTGGTTAAATCTTCATGTTGGATTAATACAGCTGCATCTATGATATCCACCA 157  
Qy 65 GAGTTAAAAAACGGTA 81  
Db 156 CCGGTAAAAAATAGTA 140

RESULT 37  
US-09-993-667-106/c  
; Sequence 106, Application US/09993667  
; Publication No. US20030022187A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kijavlin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2730P1C4  
; CURRENT APPLICATION NUMBER: US/09/993, 667  
; CURRENT FILING DATE: 2001-11-14  
; PRIOR APPLICATION NUMBER: 60/049787  
; PRIOR FILING DATE: 1997-06-16  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/065186  
; PRIOR FILING DATE: 1997-11-12  
; PRIOR APPLICATION NUMBER: 60/065311  
; PRIOR FILING DATE: 1997-11-13  
; PRIOR APPLICATION NUMBER: 60/066770  
; PRIOR FILING DATE: 1997-11-24  
; PRIOR APPLICATION NUMBER: 60/075945  
; PRIOR FILING DATE: 1998-02-25  
; PRIOR APPLICATION NUMBER: 60/078910  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/083322  
; PRIOR FILING DATE: 1998-04-28  
; PRIOR APPLICATION NUMBER: 60/084600  
; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/087106

[illegible]

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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match      27.2%; Score 28; DB 11; Length 466;
Best Local Similarity 59.7%; Pred. No. 53;
Matches 46; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

OY      5 TCACGTGCAATTAACAGCTTTATGACAGCATTAATAGCTCCTGCATATGCAATTGCTAATA 64
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      216 TGAGTGGCTTAATCATCTTTCATGCTGCGATTAATAACAGCTGCATCTATATATCCACCA 157
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY      65 CAGTTAAAAACGGTA 81
        | | ||||| |||
DB      156 CCCTGTAAAAATAGTA 140

RESULT 38
US-09-997-428-106/c
; Sequence 106, Application US/09997428
; Publication No. US20030027162A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerltzen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Guiney, Austin L.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C44
; CURRENT APPLICATION NUMBER: US/09/997,428
; CURRENT FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/087106
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02

; PRIOR APPLICATION NUMBER: 60/087609
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087759
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087827
; PRIOR FILING DATE: 1998-06-03
; PRIOR APPLICATION NUMBER: 60/088021
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088025
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088026
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; PRIOR APPLICATION NUMBER: 60/088028
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088029
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088030
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088033
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088326
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088167
; PRIOR FILING DATE: 1998-06-05
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; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088212
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088217
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088655
; PRIOR FILING DATE: 1998-06-09
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; PRIOR APPLICATION NUMBER: 60/089600
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089653
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/089907
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Query Match      27.2%;   Score 28;  DB 11;  Length 466;
Best Local Similarity 59.7%;   Pred.No. 53;
Matches 46;  Conservative 0;  Mismatches 31;  Indels 0;  Gaps 0

QY      5  TGACGCGAATTAACAGCTTTAATGACAGCATTATAGCTCCTGCATATGTAATTGCTATA 64
      111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
Db      216 TGAGTCGTGTAATATCTTTCATTCCTGCGATTAATACAGCTGCATGTATGTAATACACCA 157
QY      65 CAGTTAAAAAACGCTA 81
      1 111111 111
Db      156 CCTGTAAAAAATACTA 140

RESULT 39
US-09-997-666-106/C
; Sequence 106, Application US/09997666
; Publication No. US20030027163A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrata, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P27301PC42
; CURRENT APPLICATION NUMBER: US/09/997,666
; CURRENT FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/087106
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087609
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087759

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Query Match	27.28;	Score 28;	DB 11;	Length 466;
Best Local Similarity	59.78;	Pred. No. 53;		



;; PRIOR FILING DATE: 1998-06-19  
;; PRIOR APPLICATION NUMBER: 60/089952  
;; PRIOR FILING DATE: 1998-06-19  
;; PRIOR APPLICATION NUMBER: 60/090246  
;; PRIOR FILING DATE: 1998-06-22  
;; PRIOR APPLICATION NUMBER: 60/090252  
;; PRIOR FILING DATE: 1998-06-22  
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;; PRIOR FILING DATE: 1998-06-22  
;; PRIOR APPLICATION NUMBER: 60/090349  
;; PRIOR FILING DATE: 1998-06-23  
;; PRIOR APPLICATION NUMBER: 60/090355  
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;; PRIOR FILING DATE: 1998-06-24  
;; PRIOR APPLICATION NUMBER: 60/090431  
;; PRIOR FILING DATE: 1998-06-24  
;; PRIOR APPLICATION NUMBER: 60/090435  
;; PRIOR FILING DATE: 1998-06-24  
;; PRIOR APPLICATION NUMBER: 60/090444  
;; PRIOR FILING DATE: 1998-06-24  
;; PRIOR APPLICATION NUMBER: 60/090445  
;; PRIOR FILING DATE: 1998-06-24  
;; PRIOR APPLICATION NUMBER: 60/090472  
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;; PRIOR FILING DATE: 1998-06-24  
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;; PRIOR APPLICATION NUMBER: 60/090557  
;; PRIOR FILING DATE: 1998-06-24  
;; PRIOR APPLICATION NUMBER: 60/090676  
;; PRIOR FILING DATE: 1998-06-25  
;; PRIOR APPLICATION NUMBER: 60/090678  
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;; PRIOR APPLICATION NUMBER: 60/090690  
;; PRIOR FILING DATE: 1998-06-25  
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;; PRIOR APPLICATION NUMBER: 60/091478  
;; PRIOR FILING DATE: 1998-07-02  
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;; PRIOR FILING DATE: 1998-07-01  
;; PRIOR APPLICATION NUMBER: 60/091519  
;; PRIOR FILING DATE: 1998-07-02  
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;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091633  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091978  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/091982  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/092182  
;; PRIOR FILING DATE: 1998-07-09

Query Match 27.2%; Score 28; DB 11; Length 466;  
Best Local Similarity 59.7%; Pred. No. 53;  
Matches 46; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 5 TGACGTGAATTAACGTTTAATGACAGCATTAATAGCTCCTGATATGTGAATTCATATA 64

Db 216 TGAGTGGTTAAATCTTCAATGCGGATTAATAACAGCTGATCTATGATATCCACCA 157  
QY 65 CAGCTAAAAAACGCTA 81  
Db 156 CCCTGTAAAAAATAGTA 140

RESULT 41  
US-09-990-562-106/C  
; Sequence 106, Application US/09990562  
; Publication No. US20030027985A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Bolstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kijavrin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2730P1C18  
; CURRENT APPLICATION NUMBER: US/09/990,562  
; PRIOR FILING DATE: 2001-11-14  
; PRIOR APPLICATION NUMBER: 60/049787  
; PRIOR FILING DATE: 1997-06-16  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/065186  
; PRIOR FILING DATE: 1997-11-12  
; PRIOR APPLICATION NUMBER: 60/065311  
; PRIOR FILING DATE: 1997-11-13  
; PRIOR APPLICATION NUMBER: 60/066770  
; PRIOR FILING DATE: 1997-11-24  
; PRIOR APPLICATION NUMBER: 60/075945  
; PRIOR FILING DATE: 1998-02-25  
; PRIOR APPLICATION NUMBER: 60/078910  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/083322  
; PRIOR FILING DATE: 1998-04-28  
; PRIOR APPLICATION NUMBER: 60/084600  
; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/087106  
; PRIOR FILING DATE: 1998-05-28  
; PRIOR APPLICATION NUMBER: 60/087607  
; PRIOR FILING DATE: 1998-06-02  
; PRIOR APPLICATION NUMBER: 60/087609  
; PRIOR FILING DATE: 1998-06-02  
; PRIOR APPLICATION NUMBER: 60/087759  
; PRIOR FILING DATE: 1998-06-02  
; PRIOR APPLICATION NUMBER: 60/087827  
; PRIOR FILING DATE: 1998-06-03  
; PRIOR APPLICATION NUMBER: 60/088021  
; PRIOR FILING DATE: 1998-06-04  
; PRIOR APPLICATION NUMBER: 60/088025

;; PRIOR FILING DATE: 1998-06-04  
;; PRIOR APPLICATION NUMBER: 60/088026  
;; PRIOR FILING DATE: 1998-06-04  
;; PRIOR APPLICATION NUMBER: 60/088028  
;; PRIOR FILING DATE: 1998-06-04  
;; PRIOR APPLICATION NUMBER: 60/088029  
;; PRIOR FILING DATE: 1998-06-04  
;; PRIOR APPLICATION NUMBER: 60/088030  
;; PRIOR FILING DATE: 1998-06-04  
;; PRIOR APPLICATION NUMBER: 60/088033  
;; PRIOR FILING DATE: 1998-06-04  
;; PRIOR APPLICATION NUMBER: 60/088326  
;; PRIOR FILING DATE: 1998-06-04  
;; PRIOR APPLICATION NUMBER: 60/088167  
;; PRIOR FILING DATE: 1998-06-05  
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;; PRIOR FILING DATE: 1998-06-05  
;; PRIOR APPLICATION NUMBER: 60/088212  
;; PRIOR FILING DATE: 1998-06-05  
;; PRIOR APPLICATION NUMBER: 60/088217  
;; PRIOR FILING DATE: 1998-06-05  
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;; PRIOR FILING DATE: 1998-06-18  
;; PRIOR APPLICATION NUMBER: 60/089907  
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;; PRIOR APPLICATION NUMBER: 60/090246  
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;; PRIOR FILING DATE: 1998-06-23  
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;; PRIOR FILING DATE: 1998-06-24  
;; PRIOR APPLICATION NUMBER: 60/090435  
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;; PRIOR FILING DATE: 1998-06-24  
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;; PRIOR APPLICATION NUMBER: 60/091978  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/091982  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/092182  
;; PRIOR FILING DATE: 1998-07-09

Query Match 27.2%; Score 28; DB 11; Length 466;  
Best Local Similarity 59.7%; Pred. No. 53;  
Matches 46; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

OY 5 TGACGTGATTAACGATTATGACGATTAATGCTTCGATATGATTCCTATATA 64  
DB 216 TGAGTGTNNAAATCTTTCATGCTGCGATTAATACGCTGCATCTATGATTAATCCACCA 157



OY 65 CAGTAAAAAACGTA 81  
| | | | | | | |  
Db 156 CCCTGTAATAATAGTA 140

RESULT 42  
US-09-990-711-106/c  
; Sequence 106, Application US/09990711  
; Publication No. US2003003202A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerltsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kijavlin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paonl, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Matanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2730PIC2  
; CURRENT APPLICATION NUMBER: US/09/990,711  
; PRIOR APPLICATION NUMBER: 2001-11-14  
; PRIOR FILING DATE: 1997-06-16  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/065186  
; PRIOR FILING DATE: 1997-11-12  
; PRIOR APPLICATION NUMBER: 60/065311  
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; PRIOR APPLICATION NUMBER: 60/066770  
; PRIOR FILING DATE: 1997-11-24  
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; PRIOR FILING DATE: 1998-02-25  
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; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/083322  
; PRIOR FILING DATE: 1998-04-28  
; PRIOR APPLICATION NUMBER: 60/084600  
; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/087106  
; PRIOR FILING DATE: 1998-05-28  
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; PRIOR APPLICATION NUMBER: 60/087759  
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; PRIOR APPLICATION NUMBER: 60/088021  
; PRIOR FILING DATE: 1998-06-04  
; PRIOR APPLICATION NUMBER: 60/088025  
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; PRIOR FILING DATE: 1998-06-04

; PRIOR APPLICATION NUMBER: 60/088028  
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; PRIOR APPLICATION NUMBER: 60/088029  
; PRIOR FILING DATE: 1998-06-04  
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;; PRIOR FILING DATE: 1998-06-22  
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;; PRIOR APPLICATION NUMBER: 60/091978  
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;; PRIOR APPLICATION NUMBER: 60/091982  
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;; PRIOR APPLICATION NUMBER: 60/092182  
;; PRIOR FILING DATE: 1998-07-09

Query Match 27.2% Score 28; DB 11; Length 466;  
Best Local Similarity 59.7% Pred. No. 53;  
Matches 46; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

OY 5 TGACGAGATACAGATTAAATGACAGCATTAATAGCTCTGCATGTGGAATGCTAATA 64  
DB 216 TGAGCGGTTNAAATTTTCATGGTGAGATAATACACCTGCATCTATGATATCCACCA 157  
OY 65 CAGTTAAAAACGGTA 81  
DB 156 CCGTGTAATAAATAGTA 140

RESULT 43  
US-09-989-726-106/c  
;; Sequence 106, Application US/09989726  
;; Publication No. US20030040473A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Ashkenazi, Avi J.  
;; APPLICANT: Baker, Kevin P.  
;; APPLICANT: Botstein, David  
;; APPLICANT: Desnoyers, Luc  
;; APPLICANT: Eaton, Dan L.  
;; APPLICANT: Ferrara, Napoleone  
;; APPLICANT: Fong, Sherman  
;; APPLICANT: Gerber, Hanspeter  
;; APPLICANT: Gerltsen, Mary E.  
;; APPLICANT: Goddard, Audrey  
;; APPLICANT: Grimaldi, J. Christopher  
;; APPLICANT: Guirney, Austin L.  
;; APPLICANT: Kljavin, Ivar J.  
;; APPLICANT: Napier, Mary A.  
;; APPLICANT: Pan, James  
;; APPLICANT: Paoni, Nicholas F.  
;; APPLICANT: Roy, Margaret Ann  
;; APPLICANT: Stewart, Timothy A.  
;; APPLICANT: Tumas, Daniel  
;; APPLICANT: Watanabe, Colin K.  
;; APPLICANT: Williams, P. Mickey  
;; APPLICANT: Wood, William I.  
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
;; FILE REFERENCE: P2730PIC60  
;; CURRENT APPLICATION NUMBER: US/09/989,726  
;; PRIOR FILING DATE: 2001-11-19  
;; PRIOR APPLICATION NUMBER: 60/049787  
;; PRIOR FILING DATE: 1997-06-16  
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;; PRIOR APPLICATION NUMBER: 60/088026  
;; PRIOR FILING DATE: 1998-06-04  
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;; PRIOR FILING DATE: 1998-06-04  
;; PRIOR APPLICATION NUMBER: 60/088029

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9	PRIOR FILING DATE: 1996-06-05	
10	PRIOR APPLICATION NUMBER: 60/088202	
11	PRIOR FILING DATE: 1996-06-05	
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18	PRIOR APPLICATION NUMBER: 60/088734	
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21	PRIOR FILING DATE: 1996-06-10	
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33	PRIOR FILING DATE: 1996-06-11	
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37	PRIOR FILING DATE: 1996-06-12	
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55	PRIOR FILING DATE: 1996-06-18	
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66	PRIOR APPLICATION NUMBER: 60/090246	
67	PRIOR FILING DATE: 1996-06-22	
68	PRIOR APPLICATION NUMBER: 60/090252	
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13	PRIOR APPLICATION NUMBER: 60/090445	36
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15	PRIOR APPLICATION NUMBER: 60/090452	38
16	PRIOR FILING DATE: 1998-06-24	39
17	PRIOR APPLICATION NUMBER: 60/090542	40
18	PRIOR FILING DATE: 1998-06-24	41
19	PRIOR APPLICATION NUMBER: 60/090535	42
20	PRIOR FILING DATE: 1998-06-24	43
21	PRIOR APPLICATION NUMBER: 60/090540	44
22	PRIOR FILING DATE: 1998-06-24	45
23	PRIOR APPLICATION NUMBER: 60/090544	46
24	PRIOR FILING DATE: 1998-06-24	47
25	PRIOR APPLICATION NUMBER: 60/090552	48
26	PRIOR FILING DATE: 1998-06-24	49
27	PRIOR APPLICATION NUMBER: 60/090557	50
28	PRIOR FILING DATE: 1998-06-24	51
29	PRIOR APPLICATION NUMBER: 60/090676	52
30	PRIOR FILING DATE: 1998-06-25	53
31	PRIOR APPLICATION NUMBER: 60/090678	54
32	PRIOR FILING DATE: 1998-06-25	55
33	PRIOR APPLICATION NUMBER: 60/090680	56
34	PRIOR FILING DATE: 1998-06-25	57
35	PRIOR APPLICATION NUMBER: 60/090694	58
36	PRIOR FILING DATE: 1998-06-25	59
37	PRIOR APPLICATION NUMBER: 60/090695	60
38	PRIOR FILING DATE: 1998-06-25	61
39	PRIOR APPLICATION NUMBER: 60/090686	62
40	PRIOR FILING DATE: 1998-06-25	63
41	PRIOR APPLICATION NUMBER: 60/090865	64
42	PRIOR FILING DATE: 1998-06-26	65
43	PRIOR APPLICATION NUMBER: 60/091360	66
44	PRIOR FILING DATE: 1998-07-01	67
45	PRIOR APPLICATION NUMBER: 60/091478	68
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53	PRIOR APPLICATION NUMBER: 60/091633	76
54	PRIOR FILING DATE: 1998-07-02	77
55	PRIOR APPLICATION NUMBER: 60/091978	78
56	PRIOR FILING DATE: 1998-07-07	79
57	PRIOR APPLICATION NUMBER: 60/091982	80
58	PRIOR FILING DATE: 1998-07-07	81
59	PRIOR APPLICATION NUMBER: 60/092182	82
60	PRIOR FILING DATE: 1998-07-09	83

Query Match	27.28;	Score 28;	DB 11;	Length 466;
Best Local Similarity	59.78;	Pred. No. 53;		
Matches 46; Conservative		0; Mismatches 31;	Indels	

OY		5	TGACGTGAATTAACAGCTTTAATGACAGCAACTTATTACTCCTCATGATGCATTTGGTATATA	64
Db		216	TGAGTGSTTNAAATCTTTTCATCGTSGGATAAATAACAGCTGCATCTATGATATATCCACA	157
OY		65	CAGTTAAAAAACGGTA	81
Db		156	CCCCTTAAAAAATAGTA	140

## RESULT 44

US-09-998-156-106/C  
Sequence 106, Application US/09998156  
Publication No. US20030044806A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Bolstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730PIC28  
CURRENT APPLICATION NUMBER: US/09/998,156  
CURRENT FILING DATE: 2001-11-15  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/065186  
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PRIOR APPLICATION NUMBER: 60/090355



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43 PRIOR APPLICATION NUMBER: 60/091626
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QY	65	CAGTTAAAAAAAACGGTA	81
Db	156	CCCTGTAAAAAATAAGTA	140

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: August 25, 2003, 06:50:58 ; Search time 1644 Seconds

(without alignments)  
1522.726 Million cell updates/sec

Title: US-09-693-205A-7\_COPY\_6543\_6645

Perfect score: 103  
Sequence: 1 gaagtagcagcgaataacagf.....tccctgtctgtatccaaca 103

Scoring table: IDENTITY\_NUC  
Gapop 60.0 ; Gapext 60.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database :

EST:\*  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hic:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hic:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: em\_gss\_hum:\*  
18: em\_gss\_inv:\*  
19: em\_gss\_pln:\*  
20: em\_gss\_vrt:\*  
21: em\_gss\_fun:\*  
22: em\_gss\_man:\*  
23: em\_gss\_mus:\*  
24: em\_gss\_pro:\*  
25: em\_gss\_rtd:\*  
26: em\_gss\_phg:\*  
27: em\_gss\_vtl:\*  
28: gb\_gss1:\*  
29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	55.2	53.6	238	9	AA897178 am09e08.s.
2	55.2	53.6	713	9	AL710553 DKFZp686L
3	55.2	53.6	758	12	BM989861 UI-H-D10-
4	55.2	53.6	1010	12	BM472954 AGENCOURT

5	55.2	53.6	1083	12	BM476887	BM476887 AGENCOURT
6	46.2	44.9	1123	13	B0517082	B0517082 AGENCOURT
7	37.6	36.5	491	13	B0955705	B0955705 AGENCOURT
8	37.6	36.5	518	9	A1445627	A1445627 CJ08C05.x
9	36.2	35.1	256	12	BG898417	BG898417 HOA8-1-G1
10	36.2	35.1	507	9	A1652546	A1652546 wb61e01.x
11	36.2	35.1	534	9	A1742206	A1742206 wq39b09.x
12	36.2	35.1	607	14	CA437823	CA437823 UI-H-DHO-
13	36.2	35.1	632	13	B0772275	B0772275 UI-H-E21-
14	34.8	33.8	807	29	CNS023X0	AL180045 Telradcon
15	34	33.0	610	9	AV404852	AV404852 AV404852
16	33.8	32.8	464	14	N34305	N34305 YU51H10..s1
17	32.2	31.3	775	29	AU003905	AU003905 AUC03905
18	31.8	30.9	689	29	BX242269	BX242269 Dnlo_rer
19	31.8	30.9	760	28	BH979420	BH979420 cdf92a01.
20	31.6	30.7	858	28	B2978614	B2978614 PUG188TD
21	31.6	30.7	1088	29	B264543	B264543 CH230-458
22	31.4	30.5	802	10	BG187125	BG187125 RST6108.A
23	31	30.1	406	12	B1475987	B1475987 fp51a12.x
24	31	30.1	520	12	B1673496	B1673496 f443905.x
25	31	30.1	570	12	BM082805	BM082805 f426910.x
26	31	30.1	576	29	BX192055	BX192055 Dnlo_rer
27	30.8	29.9	175	28	AZ060239	AZ060239 RPCI-23-4
28	30.8	29.9	536	14	CA036697	CA036697 ssal10b005
29	30.8	29.9	637	14	CA064392	CA064392 ssal10b005
30	30.8	29.9	1201	13	BX339684	BX339684 BX339684
31	30.6	29.7	435	9	AW769312	AW769312 h162a09.x
32	30.6	29.7	509	28	AQ242919	AQ242919 HS_2061_A
33	30.6	29.7	525	28	AQ390562	AQ390562 CITBI-E1-
34	30.6	29.7	704	29	B2208889	B2208889 CH230-271
35	30.6	29.7	785	13	B0853968	B0853968 AGENCOURT
36	30.4	29.5	464	14	H92721	H92721 Y190H01.f1
37	30.4	29.5	702	14	CA762153	CA762153 BR060006B
38	30.4	29.5	908	29	CNS02AXT	AL189146 Telradcon
39	30.2	29.3	479	9	AM250036	AM250036 2819291.3
40	30.2	29.3	594	28	B2153139	B2153139 CH230-407
41	30	29.1	317	10	BF358120	BF358120 MR4-LT007
42	30	29.1	382	28	BH002214	BH002214 BMBAC02E1
43	30	29.1	592	28	AZ460533	AZ460533 IM0265H22
44	30	29.1	612	28	BH294981	BH294981 CH230-186
45	29.1	29.1	688	28	AZ496877	AZ496877 IM0333D03

## ALIGNMENTS

RESULT 1  
AA897178 238 bp mRNA linear EST 04-JAN-1999  
LOCUS am09e08.s1 Soares\_NFL\_T-GBC\_S1 Homo sapiens cDNA clone  
IMAGE:1466342 3', mRNA sequence.  
ACCESSION AA897178  
VERSION AA897178.1 GI:3033798  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
REFERENCE 1 (bases 1 to 238)  
AUTHORS NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL Unpublished  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
This clone is available royalty-free through LNL; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
Insert Length: 847 Std Error: 0.00  
Seq Primer: -40m13 fwd. ET from Amersham  
High quality sequence stop: 132.  
location/Qualifiers  
1..238  
/organism="Homo sapiens"

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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1466342"
/lab_host="DH10B"
/clone_lib="Soares_NFL_T-GBC_S1"
/note="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site.1: Not I; Site.2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NBHL19W, testis NHT, and B-cell NCL-GAP-GCB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bernaldo."
BASE COUNT
ORIGIN
71 a 53 c 45 g 69 t

Query Match 53.6%; Score 55.2; DB 9; Length 238;
Best Local Similarity 75.0%; Pred. No. 3.6e-05;
Matches 69; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

OY 1 GAAGTGCATGGAATAACAGCTTTAATGACAGATTAATAGCTTCGCGCAATGTGTAATGCT 60
    |||||
DB 150 GAAGTGCATGGAATAACAGCTTTAATGACAGATTAATAGCTTCGCGCAATGTGTAATGCT 91
OY 61 AATACAGTTAAATAAACGCTATTTCCCTGGTT 92
    | ||||| | || | |
DB 90 TAATACAGTTAAATAAACGCTATTTCCCTGGT 59

RESULT 2
AL710553 713 bp mRNA linear EST 22-MAR-2002
LOCUS DKEP6861236.r1.686 (synonym: hlcc3) Homo sapiens cDNA clone
DEFINITION DKEP6861236.5', mRNA sequence.
ACCESSION AL710553
VERSION AL710553.1 GI:19693908
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 713)
Ansoerge,W., Winkner,U., Mewes,W., Well,B. and Wiemann,S.
EST (Ansoerge,W., Winkner,U., Mewes,H.W., Well,B. and Wiemann,S.)
Unpublished
COMMENT
MIPS
Contact: Ansoerge W
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
Heidelberg/Germany) within the CDNA sequencing consortium of the
German Genome Project.
No sl sequence available.
This clone (DKEP6861236) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzd.de.
location/Qualifiers
1. 713
/organism="Homo sapiens"
/mol_type="mRNA"
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/clone="DKEP6861236"
/tissue_type="human skeletal muscle"
/dev_stage="adult"
/lab_host="DH10B"
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/note="Vector: pT73D-Pac; Site.1: SfiI; Site.2: SfiI;

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233 t		
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Best Local Similarity	75.0%; Pred. No. 4.3e-05;	
Matches	69; Conservative 0; Mismatches 23; Indels 0; Gaps 0;	
QY	1 GAAGTACGTCGAAATACAGTTTAAATGACAGCATTAATAGCTTCGCATATGTGAATTGCT 60	
DB	159 GAAGTACGTCGAAATACAGTTTAAATGACAGCATTAATAGCTTCGCATATGTGAATTGC 218	
QY	61 AATACAGTAAAAAAGCGTATTTCCCGGTT 92	
DB	219 TAAATACAGTAAAAAAGCGTATTTCCCGGTT 250	
RESULT 3		
BM989861	758 bp	mRNA
LOCUS	UI-H-D10-ato-m-19-0-UI.s1 NCI_CGAP_D10	linear
DEFINITION	IMAGE:5862330 3', mRNA sequence.	EST 17-JUN-2002
ACCESSION	BM989861	cdna clone
VERSION	BM989861.1	
KEYWORDS	EST.	
SOURCE	GI:19709250	
ORGANISM	Homo sapiens (human)	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
TITLE	1 (bases 1 to 758)	
JOURNAL	NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.	
COMMENT	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),	
	Tumor Gene Index	
	Unpublished	
	Contact: Robert Strausberg, Ph.D.	
	Email: cgapbs-remail.nih.gov	
	Tissue Procurement: Dr. Jose Mercuende	
	CDNA Library preparation: Dr. M. Bento Soares, University of Iowa	
	CDNA Sequencing by: Dr. M. Bento Soares, University of Iowa	
	CDNA Distribution: Clone distribution information can be found	
	through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov	
	Seq primer: M13 FORWARD	
	POLYA=Yes.	
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	/tissue_type="Lung Focal Fibrosis"	
	/dev_stage="Adult"	
	/lab_host="DH10B (Life Technologies)"	
	/clone_lib="NCI_CGAP_D10"	
	/note="Organ: Lung; Vector: p7T73-Pac (Pharmacia) with a	
	modified polylinker; Site_1: EcoR I; Site_2: Not I;	
	NCI_CGAP_D10 is a cDNA library containing the following	
	tissue(s): A pool of Lung Focal Fibrosis. The library was	
	constructed according to Bonaldo, Lennon and Soares,	
	Genome Research, 6:791-806, 1996. First strand cDNA	
	synthesis was primed with an oligo-dT primer containing a	
	Not I site. Double stranded cDNA was ligated to an EcoR I	
	adaptor, digested with Not I, and cloned directionally	
	into p7T73-Pac vector. The oligonucleotide used to prime	
	the synthesis of first-strand cDNA contains a library tag	
	sequence that is located between the Not I site and the	
	(dT)18 tail. The sequence tag for this library is	
	ATACGCGTC.	
	TAG_L1B-UI-H-D10	
	TAG_TISSUE-Lung with fibrosis	
	TAG_SEQ-ATACGCGTC"	
BASE COUNT	215 a	144 c
ORIGIN	136 g	263 t



	Query Match	53.6%:	Score 55.2:	DB 12:	Length 750;
	Best Local Similarity	75.0%:	Pred. No. 4.4e-05;		
	Matches 69;	Conservative 0;	Mismatches 23;	Indels 0;	Gaps 0;
Dy	1 GAAGTGCATCGAATAACAGTTTAATGACAGCATTAAATAGCTCCGTCAATGTAATTCCT 60       111 GAACTGACTGAATAACAGTTTAATGACAGCATTAAATAGCTCCGTCAATGTAATTCCT 170				
Dz	61 AATACTGTAAAAAACGGTATTTCCCTGCTT 92 + ++++++ - ++++++ 171 TAATACAGTTAAAAAACGGTATTTCCCTGCT 202				
RESULT 4	BMA72954	1010 bp	mRNA	linear	EST 05-FEB-2002
LOCUS	BMA72954				
DEFINITION	AGENCOURT_6466106 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:5574588				
ACCSSION	BMA72954				
VERSION	BMA72954.1	GI:18521996			
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished Contact: Robert Strausberg, Ph.D. Email: cgabbs@email.nih.gov Tissue Procurement: ATCC CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL) DNA Sequencing by: Agencourt Bioscience Corporation Genome Distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <a href="http://image.llnl.gov">http://image.llnl.gov</a> Plate: LLM12323 row: h column: 13 High quality sequence stop: 738. Location/Qualifiers 1..1010 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:5574588" /tissue_type="duodenal adenocarcinoma, cell line" /lab_host="DH10B (phage-resistant)" /note="Organ: small intestine; Vector: pCMV-SPORT6; site:1: NotI; site:2: SalI; Cloned unidirectionally; oligo-df primed. Average insert size 1.767 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH-MGC library."				
FEATURES	Source				
BASE COUNT	293 a 209 c 191 g 317 t				
ORIGIN					
Query Match	53.6%:	Score 55.2:	DB 12:	Length 1010;	
Best Local Similarity	75.0%:	Pred. No. 4.6e-05;			
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Dy	1 GAAGTGCATCGAATAACAGTTTAATGACAGCATTAAATAGCTCCGTCAATGTAATTCCT 60       111 GAACTGACTGAATAACAGTTTAATGACAGCATTAAATAGCTCCGTCAATGTAATTCCT 404				
Dz	61 AATACTGTAAAAAACGGTATTTCCCTGCTT 92 + ++++++ - ++++++ 405 TAATACAGTTAAAAAACGGTATTTCCCTGCT 436				
RESULT 5	BMA76887				

LOCUS	BM476887		1083 bp	mRNA	linear	EST-05-FEB-2002
DEFINITION	AGNCOURT_6481789 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:5555441 5' mRNA sequence.					
ACCESSION	BM476887					
VERSION	BM476887.1	GI:18525929				
KEYWORDS	EST.					
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euarchia; Primates; Carnivora; Hominoidea; Hominidae; Homo. NIH-MGC http://mgc.nci.nih.gov/ National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished					
JOURNAL	Contact: Robert Strausberg, Ph.D. Email: cgapbs@email.nih.gov Tissue Procurement: ATCC CDNA Library Preparation: Life Technologies, Inc. Agencourt Bioscience Corporation DNA Sequencing by Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <a href="http://image.lnl.gov">http://image.lnl.gov</a> Plate: LLMJ2275 row: j column: 18 High quality sequence stop: 666. Location/Organism					
FEATURES	<p>source</p> <p>1..1083</p> <p>/organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:5555441" /tissue_type="leiomyosarcoma" /_lab_host="DH10B (phage-resistant)" /_clone_id="NH_MGC_71" /note="Organ: uterus; Vector: pCMV-Sport6; Site:1: NotI; Site:2: SalI; Cloned unidirectionally. Primer: oligo dt. Average insert size 2.1 kb." Average Insert size 2.1 kb." 318 t .</p>					
BASE COUNT	334 a	219 c	212 g	318 t	.	
ORIGIN						
Query Match	53.6%	Score 55.2;	DB 12;	Length 1083;		
Best Local Similarity	75.0%;	Pred. No. 4.7e-05;				
Matches	69;	Conservative	0;	Mismatches 23;	Indels	0;
OY	1 GAAGTGACTGGAATTAACAGTTAAATGACAGCATTAAATAGCTCGCATANGAATGGCT 60	.....				
Db	617 GAAGTGACTGGAATAAACAGTTAAATGACAGCATTAAATAGCTCGCATANGAATGGC 676	.....				
OY	61 AATACAGTTAAAAAACGGTATTCCTCGGTT 92	... ....				
Db	677 TAAATACAGTTAAAAAACGGTATTCCTCGGTT 708	... ....				
RESULT 6						
LOCUS	BU517082		1123 bp	mRNA	linear	EST-12-SEP-2002
DEFINITION	AGNCOURT_10164573 NIH_MGC_71 Homo sapiens CDNA clone IMAGE:6514621 5' mRNA sequence.					
ACCESSION	BU517082					
VERSION	BU517082.1	GI:22824608				
KEYWORDS	EST.					
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euarchia; Primates; Carnivora; Hominoidea; Hominidae; Homo. NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished					
TITLE	Contact: Robert Strausberg, Ph.D. Email: cgapbs@email.nih.gov Tissue Procurement: ATCC CDNA Library Preparation: Life Technologies, Inc.					
JOURNAL						
COMMENT						

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: LLAM14090 row: d column: 14  
 High quality sequence start: 49  
 High quality sequence stop: 267.  
 Location/Qualifiers

## FEATURES

source

1. 1123  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:6514621"  
 /tissue\_type="leiomyosarcoma"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH\_MGC\_71"  
 /note="Organ: uterus; Vector: pCMV-SPORT6; Site\_1: NotI;  
 Site\_2: SalI; Cloned unidirectionally. Primer: Oligo dT.  
 Average insert size 2.1 kb."  
 BASE COUNT 283 a 336 c 194 g 310 t  
 ORIGIN

Query Match 44.9%; Score 46.2; DB 13; Length 1123;  
 Best Local Similarity 94.1%; Pred. No. 0.015;  
 Matches 48; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 GAAGTACTGATTAACAGTTAATGACAGCATTAAATAGCTCCTGCATATG 51  
 |||||  
 Db 313 GAAGTACTGATTAACAGTTAATGACAGCATTAAATAGCTCCTGCATATG 363

RESULT 7  
 BU955705/c 491 bp mRNA linear EST 21-OCT-2002  
 LOCUS AGENCOURT.10612800 NIH\_MGC\_126 Homo sapiens cDNA clone  
 DEFINITION IMAGE:6727961 5', mRNA sequence.  
 ACCESSION BU955705  
 VERSION BU955705.1 GI:24185277  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 REFERENCE NIH-MGC <http://mhc.nci.nih.gov/>.  
 1 (bases 1 to 491)  
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgaabs-r@mail.nih.gov  
 Tissue Procurement: NCI  
 CDNA Library Preparation: Michael Brownstein Laboratory  
 DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: LDCM3048 row: m column: 16  
 High quality sequence stop: 464.  
 Location/Qualifiers

## FEATURES

source

1. 491  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:6727961"  
 /tissue\_type="mixed (pool of 40 RNAs)"  
 /lab\_host="DH10B (T1-phage-resistant)"  
 /clone\_lib="NIH\_MGC\_126"  
 /note="Vector: pDNR-LIB; Site\_1: SfiI (ggccattatggcc);  
 Site\_2: SfiI (ggccgctcggcc); Double-stranded cDNA was  
 prepared from a pool of 40 cell line polyA+ RNAs (bladder  
 - 2%, blood - 33.4%, brain - 5.6%, breast - 12.5%, colon -  
 4%, connective tissue - 1.4%, eye - 1%, intestine - 2.6%,

kidney - 2.2%, liver - 5.7%, lung - 10.8%, NK-cell - 5.2%  
 , ovary - 4%, pharynx - 2.5%, prostate - 4.3%, salivary  
 gland - 1.3%, and skin - 2.3%). 5' and 3' adaptors were  
 used in cloning as follows:  
 5'-AAGCAGTGTATCAAGCAGGAGGCGCCGATAGCGCCGGC-3' and  
 5'-ATTCGTAGAGCGCGAGCGGCGCCGATAG-3'. Full-length  
 enriched library was constructed using the Clontech  
 Creator SMART kit and size-selected to contain the 0.5-1  
 kb size fraction (other fractions present in NIH\_MGC\_127  
 and NIH\_MGC\_128). Library created in the laboratory of T.  
 Udels, M.D., Ph.D. (NIMH, NIH). Note: this is a NIH\_MGC  
 Library."

BASE COUNT 161 a 75 c 81 g 159 t 15 others  
 ORIGIN

Query Match 36.5%; Score 37.6; DB 13; Length 491;  
 Best Local Similarity 61.0%; Pred. No. 3.1;  
 Matches 61; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

OY 1 GAAGTACTGATTAACAGTTAATGACAGCATTAAATAGCTCCTGCATATG 60  
 |||||  
 Db 129 GGAAGACACAAAAAATAATTCAGCATTAAGACCCCTAGAGACTTACTTTCT 70  
 OY 61 AATACGTTAAAAACGATTTCCCTGCTGTGATCCA 100  
 |||||  
 Db 69 AATCAATTAATAAAAAAGGCTTTGAGTACTTCTCATCTA 30

RESULT 8  
 A1445627 518 bp mRNA linear EST 13-APR-1999  
 LOCUS tJ08c05.x1 NCI-CGAP\_Gas4 Homo sapiens cDNA clone IMAGE:2140904 3',  
 DEFINITION mRNA sequence.  
 ACCESSION A1445627  
 VERSION A1445627.1 GI:4289534  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 REFERENCE NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
 1 (bases 1 to 518)  
 AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 JOURNAL Unpublished  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgaabs-r@mail.nih.gov  
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  
 Emmert-Buck, M.D., Ph.D.  
 CDNA Library Preparation: Life Technologies, Inc.  
 DNA Sequencing by: Greg Lennon, Ph.D.  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
[www.bio.llnl.gov/btrp/image/image.html](http://www.bio.llnl.gov/btrp/image/image.html)  
 Insert Length: 227 Std Error: 0.00  
 Seq primer: -40UP from Gibco  
 High quality sequence stop: 424.  
 Location/Qualifiers

## FEATURES

source

1. 518  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:2140904"  
 /tissue\_type="poorly differentiated adenocarcinoma with  
 signed ring cell features"  
 /lab\_host="DH10B"  
 /clone\_lib="NCI-CGAP\_Gas4"  
 /note="Organ: stomach; Vector: pCMV-SPORT6; Site\_1: SalI;  
 Site\_2: NotI; Cloned unidirectionally. Primer: Oligo dT.  
 Average insert size 1.69 kb. Life Technologies catalog #:  
 11549-011"  
 BASE COUNT 182 a 89 c 85 g 162 t

ORIGIN

Query Match 36.5% Score 37.6; DB 9; Length 518;  
 Best Local Similarity 61.0%; Pred. No. 3.1;  
 Matches 61; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

QY 1 GAAGTGCATGCAATTAACAGTTTAAATGACGATTAATAGCTCCGTCATATGTGAATGCT 60  
 Db 373 GGAAGACGCAAAAAAATTCACATTCACAGACCTAGAGACTTACTTCT 432

QY 61 AATACAGTTAAAAACGGATTTCCTGGTTCGATCA 100  
 Db 433 AATCAATTAATAAAAAAGCTTTCAGTACTTCATCTCA 472

RESULT 9  
 BG898417/c 256 bp mRNA linear EST 06-NOV-2001  
 LOCUS H0A8-1-G11 HOA (Human Osteoarthritic Cartilage) Homo sapiens cDNA,  
 mRNA sequence.  
 ACCESSION BG898417.1 GI:14308666  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J.,  
 Sathe,G., Mul,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and  
 Lark,M.W.  
 Identification and initial characterization of 5000 expressed  
 sequenced tags (ESTs) each from adult human normal and  
 osteoarthritic cartilage cDNA libraries  
 Osteoarthr. Cartil. 9 (7), 641-653 (2001)  
 JOURNAL MEDLINE 21482651  
 PUBMED 11597177  
 COMMENT Contact: Sanjay Kumar  
 UW2109  
 GlaxoSmithKline  
 709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA  
 Tel: 610-270-7245  
 Fax: 610-270-5598  
 Email: sanjay.kumar-legsk.com  
 Seq primer: T7

FEATURES  
 Location/Qualifiers  
 source  
 1..256  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /tissue\_type="cartilage"  
 /lab\_host="E.coli DH10 B"  
 /clone\_lib="HOA (Human Osteoarthritic Cartilage)"  
 /note="Vector: pSPORT I; Site\_1: SalI; Site\_2: NotI;  
 Directional"  
 BASE COUNT 61 a 56 c 54 g 85 t  
 ORIGIN

Query Match 35.1% Score 36.2; DB 12; Length 256;  
 Best Local Similarity 62.9%; Pred. No. 6.6;  
 Matches 56; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 12 AATAACAGTTATGACAGATTAAATAGCTCCGTCATATGTAATGCTTAATACAGTTAA 71  
 Db 234 AAAAAAATAATTAATTCAGATTCACAGACCCAGAGACTTACTTCTAATCAATTAA 175

QY 72 AAAAAAGTATTCCTGGTTCGATCA 100  
 Db 174 AAAAAAGTCTTCAGTACTTCATCTCA 146

RESULT 10  
 A1652546  
 Homo sapiens

LOCUS A1652546 507 bp mRNA linear EST 17-DEC-1999  
 DEFINITION wp1601.x1 NCI\_CGAP\_GC6 Homo sapiens cDNA clone IMAGE:2310168 3',  
 mRNA sequence.  
 ACCESSION A1652546  
 VERSION A1652546.1 GI:4736525  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J.,  
 Sathe,G., Mul,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and  
 Lark,M.W.  
 Identification and initial characterization of 5000 expressed  
 sequenced tags (ESTs) each from adult human normal and  
 osteoarthritic cartilage cDNA libraries  
 Osteoarthr. Cartil. 9 (7), 641-653 (2001)  
 JOURNAL MEDLINE 21482651  
 PUBMED 11597177  
 COMMENT Contact: Sanjay Kumar  
 UW2109  
 GlaxoSmithKline  
 709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA  
 Tel: 610-270-7245  
 Fax: 610-270-5598  
 Email: sanjay.kumar-legsk.com  
 Seq primer: T7

FEATURES  
 Location/Qualifiers  
 source  
 1..507  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:2310168"  
 /tissue\_type="pooled germ cell tumors"  
 /lab\_host="DH10B"  
 /clone\_lib="NCI CGAP GC6"  
 /note="Vector: pT773D-Pac (Pharmacia) with a modified  
 polylinker. Site\_1: Not I; Site\_2: Eco RI; Plasmid DNA  
 from the normalized library NCI\_CGAP\_GC4 was prepared, and  
 ss circles were made in vitro. Following HAP purification,  
 this DNA was used as tracer in a subtractive hybridization  
 reaction. The driver was PCR-amplified cDNAs from a pool  
 of 5,000 clones made from the same library (cloneds  
 1257096-1258631, 1459064-1470983, and 1475392-1476743).  
 Subtraction by Bento Soares and M. Fatima Bonaldo.  
 BASE COUNT 174 a 88 c 85 g 159 t 1 others  
 ORIGIN

Query Match 35.1% Score 36.2; DB 9; Length 507;  
 Best Local Similarity 62.9%; Pred. No. 7.5;  
 Matches 56; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 12 AATAACAGTTATGACAGATTAAATAGCTCCGTCATATGTAATGCTTAATACAGTTAA 71  
 Db 381 AAAAAAATAATTAATTCAGATTCACAGACCCAGAGACTTACTTCTAATCAATTAA 440

QY 72 AAAAAAGTATTCCTGGTTCGATCA 100  
 Db 441 AAAAAAGTCTTCAGTACTTCATCTCA 469

RESULT 11  
 A1742206  
 LOCUS A1742206 534 bp mRNA linear EST 19-DEC-1999  
 DEFINITION w339b09.x1 Soares, NSF, F8, 9W, OT, PA, P\_S1 Homo sapiens cDNA clone  
 IMAGE:2367449 3', mRNA sequence.  
 ACCESSION A1742206  
 VERSION A1742206.1 GI:5110494  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 534)  
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

JOURNAL COMMENT Unpublished  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
This clone is available royalty-free through LIND; contact the IMAGE Consortium ([infoimage.llnl.gov](http://infoimage.llnl.gov)) for further information.  
Insert length: 789 Std Error: 0.00  
Seq primer: -40UP from Glibco  
High quality sequence stop: 452.

## FEATURES

## source

1. 534  
Location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2367449"  
/lab\_host="PH10B"  
/clone\_lib="Soares\_NSF\_F8\_9W\_OT\_PA\_P\_S1"  
/note="Organ: pooled; Vector: pRT73D-Pac (Pharmacia) with a modified polylinker; Site\_1: Not I; Site\_2: Eco RI;  
Equal amounts of plasmid DNA from five normalized libraries were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 5 libraries. The pools consisted of the following libraries and clones: Soares NBHSF pool 1: 309384-310919, 323208-325895 Soares NBHP pool 1: 145032-147335, 147720-148103, 148872-149255, 15002 - 150407, 151176-152327 Soares NB2HF8-9W pool 1: 758280-760583, 772104-774407 Soares NBHPA pool 1: 304776-306311, 320136-322823, 326280-326653 Soares NBHOR pool 1: 723720-726407, 739080-740999 Subtraction by Bento Soares and M. Fatima Ronaldo."

BASE COUNT 185 a 89 c 86 g 174 t  
ORIGIN

Query Match 35.1%; Score 36.2; DB 9; Length 534;  
Best Local Similarity 62.9%; Pred. No. 7.6;  
Matches 56; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 12 AATAACAGTTAATGACAGCATTAATAGCTCGATATGTAATGCTAATACAGTTAA 71  
DB 397 AAAAAAAAAAATTCACAGCATTAACAAGACCTAGAGACTTCTTCAATCAATTAA 456  
QY 72 AAAAAAGGTATTCCTCGTCTGATCCA 100  
DB 457 AAAAAAGGTCTTCACTACTCTCATCTA 485

RESULT 12  
CA437823 607 bp mRNA linear EST 08-NOV-2002  
LOCUS CA437823  
DEFINITION UI-H-DHO-aur-o-23-0-UI.s1 NCI-CGAP\_DHO Homo sapiens cDNA clone  
ACCESSION UI-H-DHO-aur-o-23-0-UI 3', mRNA sequence.  
VERSION CA437823.1 GI:24802243  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 607)  
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
JOURNAL COMMENT Unpublished  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)

Tissue Procurement: Dr. Jose Mercuende  
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
DNA Distribution: Clone distribution information can be obtained from Dr. M. Bento Soares, [bento-soares@uiowa.edu](mailto:bento-soares@uiowa.edu)  
The following repetitive elements were found in this cDNA sequence: 1-36, >AT\_fichlow\_complexity (matched complement)  
Seq primer: M13 FORWARD  
POLYA-yes.

## FEATURES

## source

1. 607  
Location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="UI-H-DHO-aur-o-23-0-UI"  
/tissue\_type="Metastatic Chondrosarcoma"  
/dev\_stage="Adult"  
/lab\_host="PH10B (Life Technologies)"  
/clone\_lib="NCI-CGAP\_DHO"  
/note="Organ: Lung; Vector: pRT73-Pac (Pharmacia) with a modified polylinker; Site\_1: EcoR I; Site\_2: Not I;  
NCI-CGAP\_DHO is a cDNA library containing the following tissue(s): VS-8 Cell line from Metastatic Chondrosarcoma in Lung. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pRT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (GT)18 tail. The sequence tag for this library is AGATCATTCGC.  
TAG LIB=UI-H-DHO  
TAG-TISSUE=Lung  
TAG-SEQ=AGATCATTCGC"

BASE COUNT 210 a 94 c 99 g 204 t  
ORIGIN

Query Match 35.1%; Score 36.2; DB 14; Length 607;  
Best Local Similarity 62.9%; Pred. No. 7.8;  
Matches 56; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 12 AATAACAGTTAATGACAGCATTAATAGCTCGATATGTAATGCTAATACAGTTAA 71  
DB 357 AAAAAAAAAAATTCACAGCATTAACAAGACCTAGAGACTTCTTCAATCAATTAA 416  
QY 72 AAAAAAGGTATTCCTCGTCTGATCCA 100  
DB 417 AAAAAAGGTCTTCACTACTCTCATCTA 445

RESULT 13  
B0772275 632 bp mRNA linear EST 26-JUL-2002  
LOCUS B0772275  
DEFINITION UI-H-E21-bb1-k-24-0-UI.s1 NCI-CGAP\_Ch2 Homo sapiens cDNA clone  
ACCESSION UI-H-E21-bb1-k-24-0-UI 3', mRNA sequence.  
VERSION B0772275  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 632)  
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
JOURNAL COMMENT Unpublished  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
Tissue Procurement: Dr. Steven Gitellis/ Rush Presbyterian, Dept. of

FEATURES	Location/Qualifiers
source	1. .632

/note=Organ: Left Pelvis; Vector: pT773-Pac (Pharmacia) with a modified polylinker; Site-1: EcoR I; Site-2: Not I; NCL-GAP-Ch2 is a normalized cDNA library containing the following tissue(s): Chondrosarcoma Grade II. The library was constructed according to Bonaldi, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT773-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GATCAGCGT.

BASE COUNT	ORIGIN
217	a
104	c
105	g
205	t
1	others

Query Match	35.1%;	Score 36.2;	DB 13;	Length 632;
Best Local Similarity	62.9%;	Pred. NO. 7.8;		
Matches 56; Conservative	0;	Mismatches 33;	Indels 0;	Gaps 0;

QY 12 AATAACAGCTTAAAGACAGATTAAAGCTCCGCAATATGCAATTCCTAAATACAGTTAA 71  
 || || | ||| |||| | || | | |||| |  
 Db 400 AAAAAAAAAAATCCAGCATTTCAAGAGCCCTAGAGACTTACTTTCTAATCAATTAAA 459

```

QY      72 AAAAACGGTATTCCCTGGTCTGATCCA 100
        ||||| ||| ||||| | |||| |||||
Db      460 AAAAAGGCTTTCAGTACTTCTCATCTA 488

```

RESULT 14	807 bp	DNA	linear	GSS 01-SEP-2000
CNS023X0/c				
LOCUS				
DEFINITION				
CNS023X0				
Tetradodon nigroviridis genome survey sequence T7 end of clone				

233B02 of library G from *Tetradodon nigroviridis*, genomic survey sequence.

ACCESSION	AL180045
VERSION	AL180045.1
KEYWORDS	GI:7818102
	GSS: genome survey sequence.

**SOURCE**  
**ORGANISM**

REFERENCE

1. Tetradontidae, Tetraodon.

**AUTHORS**  
Roest Croallius, H., Jallion, O., Dasilva, C., Bouneau, L., Fisher, C.,  
Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F.,

**TITLE** Saurin, W. and Weissensbach, J.  
Estimate of human gene number provided by genome-wide analysis

using Tetraodon nigroviridis DNA S  
Nat. Genet. 25 (2), 235-238 (2000)

MEDLINE	20296633
PUBMED	10835645
REFERENCE	2
AUTHORS	Roest CA

**TITLE**  
Characterization and repeat analysis of the compact genome of the freshwater pufferfish *Tetraodon nigroviridis*

**JOURNAL**  
Genome Res. 10 (7), 939-949 (2000)

MEDLINE	2035983/
PUBMED	10899143
REFERENCE	3 (bases 1 to 807)

Genoscope - Centre National de Sequencage :  
Submitted (12-APR-2000)  
Direct Submission  
Genoscope.  
AUTHORS  
TITLE  
JOURNAL

BP 191 91006 EVRY cedex - FRANCE (E-mail : [segrete@genoscope.cns.fr](mailto:segrete@genoscope.cns.fr))  
- web : [www.genoscope.cns.fr](http://www.genoscope.cns.fr)  
This sequence is a single read and was generated as part of a large project of the French Genome Center.

genome. For more information, please take a look at <http://www.genoscope.cns.fr/Tetraodon>.

```

FEATURES
source
1. .807

```

```

/organism="Helicobacter nigroviridis"
/mol_type="genomic DNA"
/db_xref="taxon:99883"
/clone="233B02"
/clone_11b="G"
/note="Hemoco sequence ID : COAG3330A01LPI-end : T7"
BASE COUNT      167 a      203 c      167 g      238 t      32 others
ORIGIN

```

Query Match	33.8%	Score 34.8	DB 29	Length 807
Best Local Similarity	66.7%	Pred. No. 20		
Matches 48; Conservative	1	Mismatches 23		Indels 0

[illegible]

Qy	65	CAGTTAAAAAA	76
Db	161	AACCTAAAAAA	150

RESULT 15  
AV404852  
\*\*\*\*\*  
C10 1-1-2000  
-END  
\*\*\*\*\*  
END OF RUN 2000

LOCUS	610 bp	mRNA	linear
AV404852			
DEFINITION	Bombyx mori prothoracic gland p50 5th-Inst		
	Bombyx mori CDNA clone ppgv0517 T3, mRNA sequence		

ACCESSION	AV404852	GI:6908940
VERSION	AV404852.1	
KEYWORDS	EST.	

SOURCE	ORGANISM
Bombix mori (domestic silkworm)	Bombix mori

Eukaryota; Metazoa; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea; Bombycidae; Bombyx.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL

1 (bases 1 to 610)  
Mita, K., Moriyasu, M., Shimada, T., Okano, K. and Maeda, S  
Bombax mori cDNA  
Unpublished

**COMMENT**

Genome Research Group  
National Institute of Agrobiological Sciences  
Anagawa 4-9-1, Inaage, Chiba 263-8555, Japan  
Email: knita@nias.affrc.go.jp  
method: uni-directional, sequence direction: sequenced from T3 primer

(3) -> 3 - )  
Project= 'Silkworm Genome Program in MAFF, and Research for the  
Future Program in JSPS'. see 'Silkbase',

<http://www.ab.a.u-tokyo.ac.  
Location/qualifiers

Query Match	Best Local Similarity	Matches	Score	Pred.	DB	Length	Indels	Gaps
56; Conservative	60.2%;	0;	33.8;	37;	DB 14;	464;	0;	0;
1	GAAGTACGTGAATTAACAGCTTTAATGACAGCATTAATAGCTCCGCAATGTAATGCT	60						
372	GGAAGACGACAAAAAATAAATAAATTCAGACTTCAAGACCCAGACTTACTTTCT	431						
61	AATACAGTTAAAAAAGCGATTTTCCTCGGTTTC	93						
432	AATCATTTAAAAAAGGCTTTTCAGTACTTC	464						
RESULT 17	AU003905	775 bp	mRNA	linear	EST 19-JAN-1999			
LOCUS	AU003905	Bombyx mori p50(Daizo)	Bombyx mori	CDNA clone	ws00724,			
DEFINITION	mRNA sequence.							
ACCESSION	AU003905							
VERSION	AU003905.1	GI:4161276						
KEYWORDS	EST.							
SOURCE	Bombyx mori (domestic silkworm)							
ORGANISM	Bombyx mori							
REFERENCE	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea; Bombycidae; Bombyx.							
AUTHORS	Mita, K., Morimoto, M., Shinada, T., Okano, K. and Maeda, S.							
TITLE	Establishment of cDNA database of Bombyx mori							
JOURNAL	Unpublished							
COMMENT	Contact: Mita K Genome Research Group National Institute of Agrobiological Sciences Anagawa 4-9-1, Inage, Chiba 263-8555, Japan Email: kmita@nias.affrc.go.jp PROJECT = "CREST project by JST". Location/Qualifiers 1. 775 /organism="Bombyx mori" /mol_type="mRNA" /strain="p50(Daizo)" /db_xref="taxon:7091" /clone="ws00724" /clone_1bp="Bombyx mori p50(Daizo)"							
BASE COUNT	247 a	139 c	151 g	238 t				
ORIGIN								
Query Match	31.3%;	Score 32.2;	DB 9;	Length 775;				
Best Local Similarity	59.1%;	Pred. No. 1e+02;						
Matches	55;	Conservative	0;	Mismatches	38;	Indels	0;	Gaps
0Y	2	AAGTACTGGAATTAACAGTTAATGACAGCATTAATAGCTCCGCAATGTAATGCTA	61					
DB	94	AAGTAAAAATATACACGCTTACTGAAAGTTTAAAAAATGAAGACATGTAATGTAAT	35					
0Y	62	ATACAGTTAAAAAAGCGATTTTCCTCGGTTCT	94					
DB	34	TTAAATTACAAAACCAATTATCTAGTTT	2					

RESULT	18
LOCUS	BX242269/c 689 bp DNA linear GSS 29-JAN-2003
DEFINITION	Danio rerio genomic clone DKEX-286A22, genomic survey sequence.
ACCESSION	BX242269
VERSION	BX242269.1 GI:28164603
KEYWORDS	GSS
SOURCE	Danio rerio (zebrafish)
ORGANISM	Danio rerio
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
AUTHORS	1 (bases 1 to 689) Humphray,S.J., Huckle,E. and Durham,J.L. Direct Submission Submitted (27-JAN-2003) The Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humphraysanger.ac.uk unpublished.
COMMENT	This sequence was generated from the SP6 end of BAC 286A22. 286A22 is part of the Daniokey BAC library created by R. Plasterk and N.V. keygene. Further details: <a href="http://www.sanger.ac.uk/projects/D_rerio/">http://www.sanger.ac.uk/projects/D_rerio/</a> . Location/Qualifiers
FEATURES	1..689
SOURCE	/organism="Danio rerio" /mol_type="genomic DNA" /db_xref="taxon:7955" /clone="DKEX-286A22" /tissue_type="Testis" /note="vector pindioBAC-536"
BASE COUNT	252 a 104 c 101 g 232 t
ORIGIN	
Query Match	30.9%; Score 31.8; DB 29; Length 689;
Best Local Similarity	57.6%; Pred. No. 1,3e+02;
Matches	57; Conservative 0; Mismatches 42; Indels 0; Gaps 0;
OY	5 TGACTGCATTAACGCTTAAATGACGCAATTAAAGTCCTCGCATATGTGAATGCTATA 64
Db	428 TCACATCTCTAACGCTTTGATTAAGAAGCTAAAAAGAACATCCACTCMAAATTTACTTTT 369
OY	65 CAGTAAAAAAAAGCGTATTTCCCAGGCTTCGATCCACA 103
Db	368 ATGTTAAAAATACATAATTTTCAGGGTTTTTTTTTCACCA 330
RESULT	19
LOCUS	BH979420 760 bp DNA linear GSS 02-OCT-2002
DEFINITION	dof92a01.g1 B.oleracea002 Brassica oleracea genomic, genomic survey sequence.
ACCESSION	BH979420
VERSION	BH979420.1 GI:23462423
KEYWORDS	GSS.
SOURCE	Brassica oleracea
ORGANISM	Brassicaceae
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids ; eurosids II; Brassicales; Brassicaceae; Brassica.
AUTHORS	1 (bases 1 to 760) Delehaunty,K., Fewell,G., Fulton,L., McCombie,W.R., Miner,T., Nash ,W., Raboinowicz,P.D. and Wilson,R.K. Whole genome shotgun reads from Brassica oleracea
TITLE	Contact: Richard K. Wilson
JOURNAL	Genome Sequencing Center Unpublished Washington University School of Medicine Email: submissions@watson.wustl.edu Plate: dof92 row: a column: 01 Seq primer: -28RPOT reverse Class: shotgun
COMMENT	High quality sequence start: 104 High quality sequence stop: 779.

```

FEATURES
Source
    Location/Qualifiers
    1..760
    /organism="Brassica oleracea"
    /mol_type="genomic DNA"
    /db_xref="taxon:3712"
    /clone_lib="B.oleracea002"
    /note="Vector: pOTw13; Whole genome shotgun library from flowering buds. DNA was purified from a crude nuclear prep using Brassica oleracea T01000DH3 buds provided by Thomas Osborn at the University of Wisconsin. Genomic DNA was provided by Pablo Rabinowicz (CSHL) and the shotgun library prepared at Washington University Genome Sequencing Center."

BASE COUNT
    264 a 171 c 106 g 219 t

ORIGIN
Query Match 30.9%; Score 31.8; DB 28; Length 760;
Best Local Similarity 59.3%; Pred. No.1.3e+02;
Matches 54; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY 13 ATACAGCTTTAATGACAGCATTAATAGCTCCGATATGTGAATTGCTAATACAGTTAAA 72
    |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| | ||||
Db 157 ATAAATCTTGATGATGAATAAATTAAGTAGTTCCATAAATATTAATTAATTAACATATA 216

QY 73 AAAACGATTTTCCCTGCTGTCTGATCCACA 103
    | || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 217 ATAACTCCACTTTCGTGATCTTTTACAACA 247

RESULT 20
B2978614/c 858 bp DNA linear GSS 25-MAR-2003
LOCUS
DEFINITION
    PUGIJB8TD ZM.0_6_1.0_KB zea mays genomic clone ZMWBta391008,
    genomic survey sequence.
ACCESSION
    B2978614
VERSION
    B2978614.1 GI:29207563
KEYWORDS
    GSS.
SOURCE
    zea mays
    zea mays
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
    clade; Panicoideae; Andropogoneae; Zea.
    1 (bases 1 to 858)
    Whitelaw,C.A., Quackenbush,J., Van Aken,S., Uterback,T., Resnick
    A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and Bennetzen,J.
    Maize Genomics Consortium
    Unpublished
    Other_GSSs: PUGIJB8TB
    Contact: Cathy Whitelaw
    TIGR
    9712 Medical Center Drive, Rockville, MD 20850, USA
    Tel: 301-838-5843
    Fax: 301-838-0208
    Email: whitelaw@tigr.org
    Seq Primer: TF
    Class: sheared ends.

FEATURES
Source
    Location/Qualifiers
    1..858
    /organism="Zea mays"
    /mol_type="genomic DNA"
    /strain="B73"
    /db_xref="taxon:4577"
    /clone="ZMWBta391008"
    /clone_lib="ZM.0_6_1.0_KB"
    /note="Vector: pCR4-topo; Site 1: EcoRI; 0.6-1.0 kb high
    Cot selected genomic DNA library"

BASE COUNT
    266 a 175 c 157 g 260 t

ORIGIN
Query Match 30.7%; Score 31.6; DB 29; Length 858;
Best Local Similarity 60.5%; Pred. No.1.6e+02;
Matches 52; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

```





TITLE	Washu Zebrafish EST Project 1998
JOURNAL	Unpublished
COMMENT	Other_ESTS: ft43g05.y1
	Contact: Stephen L. Johnson

TITLE  
JOURNAL  
COMMENT

and Wilson, R.  
Washu Zebrafish EST Project  
Unpublished  
Contact: Stephen L. Johnson

Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: zbrafish@wustl.edu

CDNA Library constructed by library constructed by Invitrogen and  
donated by R. Campbell (Marine Biology Laboratory, Woods Hole, MA).  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: the I.M.A.G.E. Consortium/LNL, send email to:  
info@image.llnl.gov

High quality sequence stop: 401.

#### FEATURES

source

Location/Qualifiers

1..570

/organism="Danio rerio"

/mol\_type="mRNA"

/db\_xref="taxon:7955"

/clone="IMAGE:5306682"

/sex="female"

/dev\_stage="4-5 months, 1 year and 2 years"

/lab\_host="DH10B (phage-resistant)"

/clone\_lib="Campbell zebrafish ovary"

/note="Organ: ovary (pooled); Vector: pCMV-Sport6; Site: 1:  
NotI; Site 2: SalI; Whole ovaries collected from zebrafish  
aged 4-5 months, 1 year and 2 years. Oligo-dT primed,  
directionally cloned. Average insert size 2 kb. Library  
constructed by Invitrogen and donated by R. Campbell  
(Marine Biology Laboratory, Woods Hole, MA)."

#### BASE COUNT

195 a 114 c 91 g 170 t

#### ORIGIN

Query Match

Best Local Similarity 57.9%; Score 31; DB 12; Length 570;  
Pred. No. 2.1e+02;

Matches 55; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

9 TGGAAATACAGTTTAAATGACAGCATTATAGCTCTGCAATGATGCTAATACACT 68

146 TGGAAATACAGTTTAAATGACAGCAGGGCTTAAAGCTCCCGCTTAAACAAAGCATGCTCT 205

69 TAAAAAAGCGTATTTCCCTGCTTGCATCAACA 103

206 TACACACCGCAATATCATCATATTAATA 240

Db

#### RESULT 26

BX192055 576 bp DNA linear GSS 13-MAR-2003

DEFINITION Danio rerio genomic clone DKEY-203G4, genomic survey sequence.

ACCESSION BX192055

VERSION BX192055.1 GI:28023941

KEYWORDS GSS.

SOURCE Danio rerio (zebrafish)

ORGANISM Danio rerio

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;

Cypriniformes; Cyprinidae; Danio.

1 (bases 1 to 576)

Humphray, S.J., Huckle, E. and Durham, J.L.

Direct Submission

Submitted (13-MAR-2003) The Sanger Institute, Wellcome Trust Genome  
Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:  
humphray@sanger.ac.uk Unpublished

This sequence was generated from the SP6 end of BAC 203G4. 203G4 is  
part of the Daniokey BAC Library created by R. Plasterk and N.V.

Keygene. Further details:  
[http://www.sanger.ac.uk/Projects/D\\_rerio/](http://www.sanger.ac.uk/Projects/D_rerio/).

Location/Qualifiers

1..576

/organism="Danio rerio"

/mol\_type="genomic DNA"

/db\_xref="taxon:7955"

/clone="DKEY-203G4"

/tissue\_type="Testis"

/note="vector pIndigOBAC-536"

#### FEATURES

source

BASE COUNT 188 a 125 c 97 g 166 t

#### ORIGIN

Query Match 30.1%; Score 31; DB 29; Length 576;  
Best Local Similarity 57.9%; Pred. No. 2.1e+02;

Matches 55; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

9 TGGAAATACAGTTTAAATGACAGCATTATAGCTCTGCAATGATGCTAATACACT 68

54 TGGAAATACAGTTTAAATGACAGGGCTTAAAGCTCCCGCTTAAACAAAGCATGCTCT 113

69 TAAAAAAGCGTATTTCCCTGCTTGCATCAACA 103

114 TACACACCGCAATATCATCATATTAATA 148

Db

#### RESULT 27

AZ060239/c

LOCUS

RPCT-23-41AG20.TV RPCT-23 Mus musculus genomic clone RPCT-23-41AG20

DEFINITION , genomic survey sequence.

ACCESSION AZ060239.1 GI:7351488

VERSION GSS.

KEYWORDS Mus musculus (house mouse)

SOURCE Mus musculus

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 175)

Zhao, S., Niernan, W., Feldblyum, T., Malek, J., Shatsman, S., Akintet,

B., Levins, M., McGann, S., Tsegaye, G., Geer, K., Krol, M., de Jong, P.

and Fraser, C.M.

Mouse BAC End Sequences from Library RPCT-23

Unpublished

Other GSSs: RPCT-23-41AG20.TJ

Contact: Shaying Zhao

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0208

Fax: 301 838 0208

Email: szhao@tigr.org

Clones are derived from the mouse BAC library RPCT-23. For BAC

library availability, please contact Pieter de Jong

(pieter@dejong.med.bufileo.edu). Clones may be purchased from

BACPAC Resources (<http://bacpac.med.bufileo.edu/orderframe.htm>)

or from Resea.ch Genetics (info@resga.com). BAC end page:

[http://www.tigr.org/tdb/bac/ends/mouse/bac\\_end\\_intro.html](http://www.tigr.org/tdb/bac/ends/mouse/bac_end_intro.html)

Plate: 414 row: 6 column: 20

Seq primer: T7

Class: BAC ends.

Location/Qualifiers

1..175

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="RPCT-23-41AG20"

/sex="Female"

/lab\_host="DH10B"

/clone\_lib="RPCT-23"

/note="Organ: Kidney/Brain; Vector: pBAC3.6; Site: 1:  
EcoRI; Site 2: EcoRI; Female C57BL/6J mouse kidney and/or  
brain genomic DNA was isolated and partially digested  
with a combination of EcoRI and EcoRI Methyase. Size  
selected DNA was cloned into the pBAC3.6 vector at the  
EcoRI sites. The ligation products were transformed into  
DH10B electrocompetent cells (BRL Life Technologies)."

#### BASE COUNT

53 a 21 c 35 g 66 t

#### ORIGIN

Query Match

Best Local Similarity 58.9%; Score 30.8; DB 28; Length 175;  
Pred. No. 1.9e+02;

Matches	53:	Conservative	0:	Mismatches	37:	Indels	0:	Gaps	0:
QY	14	TAACAGTTTAATGACACCAATTAACTAGCTCTGCATANGAATGCTTAATACACTTAAAA	73						
Db	134	TAACATTTTAATGAGTCTTGAAAAAAATTTCAAAATTCATCTAGATGAAATTAAGT	75						
QY	74	AAAGCGATTTCCCTGCTTGACGCCAACA	103						
Db	74	AAGCAATTTTCACCTCTCTCATAAACA	45						
RESULT 28									
LOCUS	CA036697/c	536 bp	mRNA	linear	EST 04-MAR-2003				
DEFINITION	salidb005008	reproductive Salmo salar cDNA, mRNA sequence.							
ACCESSION	CA036697								
VERSION	CA036697.1	GI:24335681							
KEYWORDS	EST.								
SOURCE	Salmo salar (Atlantic salmon)								
ORGANISM	Salmo salar								
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Proteoanchopterygii; Salmoniformes; Salmonidae; Salmo.								
AUTHORS	1 (bases 1 to 536) GRASP Consortium, Davidson, W.S., Koop, B.F. and http://web.vic.ca/cbr/grasp.								
TITLE	A survey of Salmo salar transcripts from high complexity cDNA libraries								
JOURNAL	Unpublished								
COMMENT	Contact: Koop BF Centre for Biomedical Research University of Victoria PO Box 3020 STN CSC, Victoria BC, V8W 3N5, Canada Tel: 250 472 4067 Fax: 250 472 4075 Email: bkoop@vic.ca Centre for Biomedical Research, University of Victoria cDNA preparation and sequencing: Roberto Alberto, Marianne Beetz-Sargent, Maura Busby, Peter Hunt, Linda McKinnel, BF Koop. bioinformatics: Gordon D Brown POLYA-yes.								
FEATURES	Location/Qualifiers								
source	1..536								
	/organism="Salmo salar"								
	/mol_type="mRNA"								
	/strain="McConnell"								
	/db_xref="taxon:8030"								
	/clone_id="reproductive"								
	/note="Vector: pluescriptITLTK+; Library Creator: Kristian R von Schalburg; Atlantic salmon tissue contributors: Carlo Biagi, Mitch Uh and Robert Devlin (DFO), Vancouver, B.C.), Simon Jones (PBS, Nanaimo, B.C.), Seespring Hatchery (Crofton, B.C.), Rachel Roper (University of Victoria)"								
BASE COUNT	173 a 116 c 84 g 163 t								
ORIGIN									
Query Match	29.9%	Score 30.8;	DB 14;	Length 536;					
Best Local Similarity	61.0%;	Pred. NO. 2.4e+02;							
Matches	50:	Conservative	0:	Mismatches	32:	Indels	0:	Gaps	0:
QY	2	AAGTACGTGAATGACCACTTAATGAGCTTCCTGCATATGCAATGCAATGCGTA	61						
Db	91	AAGGATGTTGTAATTAACGAGATCACTAATGATGTTGTTTGTATCTGCTGAATGTA	32						
QY	62	ATACAGTTAAAAAAGCGTATT	83						
Db	31	ATACATCAAAATACCAAGTTT	10						
RESULT 29									

CA064392/c	CA064392	637 bp	mrna	linear	EST 04-MAR-2003
LOCUS	salalr5b5.4124 mixed_tissue Salmo salar cDNA, mRNA sequence.				
DEFINITION	CA064392				
ACCESSION	CA064392.1	GI:24394635			
VERSION	EST				
KEYWORDS	Salmo salar (Atlantic salmon)				
SOURCE	Salmo salar				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.				
REFERENCE	1 (bases 1 to 637)				
AUTHORS	GRASP Consortium, Davidson, W.S., Koop, B.F. and http://web.uvic.ca/cbr/grasp.				
TITLE	A survey of Salmo salar transcripts from high complexity cDNA libraries				
JOURNAL	Unpublished				
COMMENT	Contact: Koop BF Centre for Biomedical Research University of Victoria PO Box 3020 STN CSC, Victoria BC, V8W 3N5, Canada Tel: 250 472 4067 Fax: 250 472 4075 Email: bkoop@uvic.ca Genome Sciences Centre, BC Cancer Agency cDNA preparation, sequencing and bioinformatics: Y Butterfield, R Kirkpatrick, J Asano, N Gilm, R Gilm, D Lee, S Lee, T Olson, P Pandoh, A Prabhu, D Smallus, L Spence, J Stott, S Taylor, G Yang, J Schein, S Jones and M Marra. Location/Qualifiers 1..637 /organism="Salmo salar" /mol_type="mrna" /strain="MocConnell" /db_xref="taxon:8030" /clone_lib="mixed_tissue" /note="Vector: pCMVSPORT6; Library Creator: Research Genetics ; Atlantic salmon tissue contributors: Carlo Biagi, Mitch Uh and Robert Devlin (DFO, Vancouver, B.C.), Simon Jones (PBS, Nanaimo, B.C.), Seespring Hatchery (Crofton, B.C.), Rachel Roper (University of Victoria)"				
BASE COUNT	212 a 132 c 97 g 196 t				
ORIGIN					
	Query Match	29.9%	Score 30.8;	DB 14;	Length 637;
	Best Local Similarity	61.0%;	Pred. NO. 2.5e+02;		
	Matches	50;	Conservative	0;	Mismatches 32; Indels 0; Gaps 0;
OY	2 AAGTACTGCAATACAGCTTTAATGACAGCATTAATAGCTCCTCGCATATGTAATGCTA	61			
DB	243 AAGTCATTTGTAATACAGGATACATGATGATGTTTGTATCTGCTGTAAATGTA	184			
OY	62 ATACAGTTAAAAAAGCGTATT	83			
DB	183 ATACATCAAAATACCAAGCTTT	162			
RESULT 30					
LOCUS	BX339684	1201 bp	mrna	linear	EST 02-MAY-2003
DEFINITION	BX339684 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CSOD1075YB16 5-PRIME, mRNA sequence.				
ACCESSION	BX339684				
KEYWORDS	BX339684.1	GI:30341837			
SOURCE	EST				
ORGANISM	Homo sapiens (human)				
	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1 (bases 1 to 1201)				
AUTHORS	Li, W.B., Gruber, C., Jessee, J. and Polayes, P.				
TITLE	Full-length cDNA libraries and normalization				
JOURNAL	Unpublished				





Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800

```

FEATURES
source      location/Qualifiers
1. 702     /organism="Oryza sativa (indica cultivar-group)"

```

```

/mol_type="mRNA"
/db_xref="taxon:39946"
/clone="BR060006B20E09.ab1"
/tissue_type="Panicles"
/dev_stage="Flowering"
/clone_lib="IRRI clones"
/notes="Vector: pBluescript II SK+; Water stress was
applied by not watering for 4 consecutive days. Panicles
were collected from control (well watered) and stressed
plants at 2 days before heading, heading, 50% flowering
and 4 days after 50% flowering."

BASE COUNT      205 a      151 c      132 g      214 t
ORIGIN

Query Match      29.5%; Score 30.4; DB 14; Length 702;
Best Local Similarity 67.2%; Pred. No. 3.2e+02;
Matches 43; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY      13 ATACAGTTTATGACGATTATAGCTTCGATATGGAATTCCTAATACGTTAA 72
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB      73 ATACAGATTACTGATTAATCTAATATATGATGCTGATATTTGAGATCAAAAAA 14
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY      73 AAAA 76
      ||||
DB      13 AAAA 10

RESULT 38
CNS02AXT/LOCUS      908 bp      DNA      linear      GSS 01-SEP-2000
DEFINITION      Tetradon nigriviridis genome survey sequence PUC-Or1 end of clone
                252F17 of library G from Tetradon nigriviridis, genomic survey
                sequence.
ACCESSION      AL189146
VERSION      AL189146.1 GI:7827250
KEYWORDS      GSS: genome survey sequence.
SOURCE      Tetradon nigriviridis
ORGANISM      Tetradon nigriviridis
                Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
                Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
                Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
                Tetraodontidae; Tetraodon.
REFERENCE      1 Roest Crolius, H., Jallion, O., Dasilva, C., Bouneau, L., Fisher, C.,
                Bernot, A., Fitzames, C., Wincker, P., Brothier, P., Quetier, F.,
                Sautin, W. and Weissenbach, J.
                Estimate of human gene number provided by genome-wide analysis
                using Tetradon nigriviridis DNA sequence
                Nat. Genet. 25 (2), 235-238 (2000)
JOURNAL      20296633
MEDLINE      10835645
PUBMED
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
COMMENT
This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetradon nigriviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/tetradon.
FEATURES
source      1..908

```

```

/organism="Tetradon nigriviridis"
/mol_type="genomic DNA"
/db_xref="taxon:99883"
/clone="252F17"
/clone_lib="G"
/notes="Genoscope sequence ID : C0AG252CC09SP1-end :
PUC-Or1"

BASE COUNT      286 a      176 c      212 g      233 t      1 others
ORIGIN

Query Match      29.5%; Score 30.4; DB 29; Length 908;
Best Local Similarity 59.8%; Pred. No. 3.4e+02;
Matches 49; Conservative 1; Mismatches 32; Indels 0; Gaps 0;

QY      6 GACTGAAATACAGTTTATGACGATTAATAGCTTCGATATGGAATTCCTAATAC 65
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB      907 GACTGATTAATAATTTATCTAATATTAATTTAGGCTTGTATTAATCTTAATTC 848
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY      66 AGTTAAAAAAGCGTATTTCCC 87
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB      847 ATCTCAATTAACCGTATTTGCC 826
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 39
AM250036/LOCUS      479 bp      mRNA      linear      EST 07-JAN-2000
DEFINITION      2819291.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2819291 3',
                mRNA sequence.
ACCESSION      AM250036
VERSION      AM250036.1 GI:6593029
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE      1 (bases 1 to 479)
                NIH-MGC http://mgc.nci.nih.gov/
                National Institutes of Health, Mammalian Gene Collection (MGC)
                Unpublished
                Other ESTs: 2819291.5prime
                Contact: Robert Strausberg, Ph.D.
                Email: cgaps-remail.nih.gov
                Tissue Procurement: DCTD/DRP cDNA library preparation: Ling
                Hong/Rubin Laboratory cDNA library Arrayed by: The I.M.A.G.E.
                Consortium (LNL) DNA Sequencing by: Berkeley MGC sequencing
                project Clone distribution: MGC clone distribution information can
                be found through the I.M.A.G.E. Consortium/LNL at:
                www.bio.lnl.gov/brp/image/image.html Base Calling / Quality
                Scores: PHRED from University of Washington Genome Center. Vector
                trimming: cross-match from University of Washington Genome Center
                PHRAP suite. Poly-T identification: patmatch.pl from Berkeley
                Drosophila Genome Project. University of Washington Genome Center:
                http://www.genome.washington.edu/polyadenylation: Based upon the
                presence of a XhoI site followed by a run of 14 or more T residues
                at the beginning of the sequence, this cDNA insert was
                polyadenylated.
                Plate: LCCM row: D column: 12
                High quality sequence stop: 376.
                Location/Qualifiers
                1..479
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="IMAGE:2819291"
                /tissue_type="small cell carcinoma"
                /cell_line="MGC3"
                /lab_host="DH10B (phage-resistant)"
                /clone_lib="NIH_MGC_7"
                /note="Organ: lung; Vector: pORF7; Site_1: XhoI; Site_2:
                EcoRI; cDNA made by oligo-dT priming. Directionally
                cloned into EcoRI/XhoI sites using the following 5'
                adaptor: GGCACGAG(G). Size-selected >500bp for average
                insert size 1.8kb. Library constructed by Ling Hong in

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[illegible]

AZ460533/C		592 bp	DNA	linear	GSS 04-OCT-2000
LOCUS					
DEFINITION	IM0265H2R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0265H2 R, genomic survey sequence.				
ACCESSION	AZ460533				
VERSION	AZ460533.1	GI:10618658			
KEYWORDS	GSS.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Cranialta; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
AUTHORS	I (bases 1 to 592) Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmood,R., Meenen,E., Pedersen,T., Rilly ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts Unpublished Contact: Robert B. Weiss University of Utah Genome Center Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA Tel.: 801 585 5606 Fax: 801 585 7177 Email: ddunne@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0265 row: H column: 22 Seq primer: CACACGAGAAACACGTATGACC Class: plasmid ends High quality sequence stop: 592.				
FEATURES	Location/Qualifiers				
Source	1..592 /organism="Mus musculus" /mol_type="genomic DNA" /strain="C57BL/6J" /db_xref="taxon:10090" /clone="UUGC1M0265H22" /sex="Male" /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-" /clone_lib="Mouse 10kb plasmid UUGC1M library" /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource ( <a href="http://www.jax.org/resources/documents/dnares/">http://www.jax.org/resources/documents/dnares/</a> ). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD2 (gi14732114 gb AF129072.1), a copy-number inducible derivative of plasmid RL. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance.				
BASE COUNT	179 a 145 c 111 g 156 t				1 others
ORIGIN					
Query Match	29.1%; Score 30;	DB 28;	Length 592;		
Best Local Similarity	67.7%;	Pred. No. 4e+02;			
Matches	Conservative 0;	Mismatches 20;	Indels 0;	Gaps 0;	
OY	28 CAGCATTAATAGCTGCATATGTGAATTCCTAATACATTAAAAAACGGTATTCC 87				
DB	133 CAGCATTAAGATATACATGCATAAATTAATTTCCCAATCCAGTTACAACAAGCATTTGCG 74				
OY	88 TG 89				

[illegible]

ACCESSION	clone UGCG1M0333D03 R, genomic survey sequence.
VERSION	AZ496877
KEYWORDS	AZA96877.1 GI:10673385
SOURCE	GSS.
ORGANISM	Mus musculus (house mouse)
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS	Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
TITLE	1 (bases 1 to 688)
JOURNAL	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamll,C.,
COMMENT	Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
	,M., Rose,M., Rogase,R., Stokes,R., Tingey,A., von Niederhausen,A.
	and Wright,D., Weiss,R.
	Mouse whole genome scaffolding with paired end reads from 10kb
	plasmid inserts
	Unpublished
	Contact: Robert B. Weiss
	University of Utah Genome Center
	University of Utah
	Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLc, UT
	84112, USA
	Tel.: 801 585 5606
	Fax: 801 585 7177
	Email: ddunne@genetics.utah.edu
	Insert Length: 10000 Std Error: 0.00
	Plate: 0333 row: D column: 03
	Seq primer: CACACAGAAACAGCTATGACC
	Class: plasmid ends
	High quality sequence stop: 688.
FEATURES	
Source	Location/Qualifiers
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	/organism="Mus musculus"
	/mol_type="genomic DNA"
	/strain="C57BL/6J"
	/db_xref="taxon:10090"
	/clone="UGCG1M0333D03"
	/sex="male"
	/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
	/clone_lib="Mouse 10kb plasmid UGCG1M library"
	/note="Vector: PWD42nv: Purified genomic DNA from M.
	musculus C57BL/6J (male) was obtained from the Jackson
	Laboratory Mouse DNA Resource
	(http://www.jax.org/resources/documents/dnares/). The DNA
	was hydrodynamically sheared by repeated passage through a
	0.005 inch orifice at constant velocity. The sheared DNA
	was blunt end-repaired with T4 DNA polymerase and T4
	polynucleotide kinase. Adaptor oligonucleotides were
	ligated to the blunt ends in high molar excess. The
	adapted DNA was purified and size-selected for a 9.5 to
	10.5 kb range using preparative agarose gel
	electrophoresis. Vector DNA was prepared from a derivative
	of pMDA2 (gil4732114[gb]/AF129072.1), a copy-number
	inducible derivative of plasmid RL. The vector was ligated
	with adaptors complementary to the insert adaptors and
	purified. The sheared, adapted mouse DNA was annealed to
	adapted vector DNA, and transformed into
	chemically-competent E. coli XL10-Gold (Stratagene) cells
	and selected for ampicillin resistance."
BASE COUNT	191 a 142 c 123 g 231 t 1 others
ORIGIN	
Query Match	29.1%; Score 30; DB 28; Length 688;
Best local Similarity	57.4%; Pred. No. 4.2e+02;
Matches	54; Conservative 0; Mismatches 40; Indels 0; Gaps 0;
OY	5 TGACTGAATAACAGTTTAATGACCATTAATAGCTCTGCATFATGTGAATTGCTAATA 64
DB	437 TAACAGAGATTATAGTGTTCCTAACCCATCATATATAAATGCACTGACACTACAGCTCTAGA 378
OY	65 CAGTTAAAAAAGCGTATTTCCCTGGTTCGATC 98
DB	377 CAGAAAAANAATCTGACTGTCTCTGATGCTCTTC 344

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Search completed: August 25, 2003, 07:49:37  
Job time : 1653 secs

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